



; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: JP 2001-379298  
; PRIORITY FILING DATE: 2001-11-05  
; NUMBER OF SEQ ID NOS: 4996  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1958  
; LENGTH: 2508  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-11-072-512-1958

Alignment Scores:  
pred. No.: 5 33e-127 Length: 2508  
Score: 1492.50 Matches: 275  
Percent Similarity: 74.2% Conservative: 36  
Best Local Similarity: 65.6% Mismatches: 65  
Query Match: 64.7% Indels: 43  
Db: 9 9 Gaps: 4

US-10-041-030-4 (1-420) x US-11-072-512-1958 (1-2508)

Qy 3 SerProGlyGlnGluGluHisCysAlaProAlaSerGluProAlaValTyrGlyGluLeu 22  
Db 208 TCTCCCCGGCTCTGAGATGGCGACGCCGAGCCCTCAACTATGTGACTC 261  
Qy 23 ValValLeuGlyTyrAsnGlyAlaLeuProAsnGlyAspArgGlyArgArgIleSerArg 42  
Db 261 -  
Qy 43 PheAlaLeuTyrIleAspArgProLysAlaAsnGlyAlaProSerThrValIleValIle 62  
Db 262 -  
Db 63 SerPheProGlnAlaSerIleSerCysAlaGlyGlnIleSerIleSerTyrThr 82  
Db 265 TCCAGCGCCGCTCGTCCAGGCTACTGACTAACGGTGGTCAGCAAGCTCTATCA 324  
Qy 83 LeuSerAlaGangIleThrValValValGlyTyrThrIleAspThrAspMetPhe 102  
Db 325 CTCTCCCGGAGGACTCTGGTAACTGAGCTACAGTGATGGCACACAAGATGTC 384  
Qy 103 GluValGlyArgSerThrGluSerProIleAspPheValValThrAspThrIleSerGly 122  
Db 385 CAGAATGGCCGCTTCAAGAGAACATGATGACTCTGGTAACTGAGACA 444  
Qy 123 SerGlnAnthrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAlaCysArg 142  
Db 445 GGA---GGGGCTCCGAGGAGGCGCCCTCTGCGCCATCTCCGCG 501  
Qy 143 IleValCysBspArgAsnGluProTyrThrAlaArgIlePheAlaAlaGlyPheAspSer 162  
Db 502 ATCCCTCTGAGCCGGCCACCTATACTGCCGCATCTACCGCTGGCTGATCC 561  
Qy 163 SerGlyAsnIlePheIleLeuGlyIleValAlaIleSerIleSerAspGlyIleMet 182  
Db 562 TCTAGCAACATCTCTGGAGACGGAGGCCAAATGGGACCCAGATGGCTGATG 621  
Qy 183 AspGlyLeuThrThrAspGlyValleValMetIleProArgGlyGlyPheThrGlu 202  
Db 622 GATGGACTCTGACCACTGGATGAGTCACCGGGAGCGCTCTCCGAGAC 681  
Qy 203 SerGlnProGlyValTrpArgGluIleSerValCysGlyAspValTyrThrLeuArgGlu 222  
Db 682 TCAACCCGGGCTCTGGGGAGATCTGGCTCTGGGAAATGTGACATGGGGAC 741  
Qy 223 ThrArgSerAlaGlnGlnArgGlyIleLeuValIleSerGlnIleThrValIleAsp 242  
Db 742 AGGGCTCTGACCGAGCGGGCAAGCTGGTGAAGAACGAGTCACGTGCGAGAC 801  
Qy 243 GlySerLeuIleAspLeuGlyValIleLeuTrpArgThrAlaAspGlyLeupe 262  
Db 802 GGCTCTCTCATGACCTGTTGGCTGCGCAACCGCGGGCTG 861

RESULT 2  
US-10-750-185-40960/c  
; Sequence 40960, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, SUE K.  
; APPLICANT: KERR, RICHARD  
; APPLICANT: ROSENFIELD, DAVID  
; APPLICANT: HOLM, TOM  
; APPLICANT: BATES, STEPHEN  
; APPLICANT: FANTIN, DENNIS  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; PRIORITY APPLICATION NUMBER: US 60/437,482  
; PRIORITY FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40960  
; LENGTH: 1105  
; TYPE: DNA  
; ORGANISM: Bovine 19866880722813  
; US-10-750-185-40960

Alignment Scores:  
Pred. No.: 4 41e-56 Length: 1105  
Score: 711.50 Matches: 164  
Percent Similarity: 66.9% Conservative: 48  
Best Local Similarity: 51.7% Mismatches: 97  
Query Match: 31.1% Indels: 12  
Db: 8 8 Gaps: 4

US-10-041-030-4 (1-420) x US-10-750-185-40960 (1-1105)

Qy 108 ThrGluSerProIleAspPheValValThrAspThrIleSerGlySerGlnAnthrAsp 127  
Db 1102 ACTGAACACTCTCATTAATTGTGATACTGATGATGATGTCAGGAT-TAAAGTATGAT 1044  
Qy 128 -----GluAlaGlnIleThrGlnSerThrIleSerArgPheAlaCysArgIleValCys 145



RESULT 4  
US-09-925-065A-679103  
; Sequence 679103, Application US/09925065A  
; Publication No. US2004018104BA1  
; GENERAL INFORMATION:  
; APPLICANT: WANG, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827-135  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243, 096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252, 147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250, 092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261, 766  
; PRIOR FILING DATE: 2000-01-16  
; PRIOR APPLICATION NUMBER: US 60/389, 846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 937086  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 679103  
; LENGTH: 1345  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-925-065A-679103  
Alignment Scores:  
Pred. No.: 2.86e-17 Length: 1345  
Score: 293.00 Matches: 80  
Percent Similarity: 49.2% Conservative: 17  
Best Local Similarity: 40.6% Mismatches: 50  
Query Match: 12.8% Indels: 53  
DB: 6 Gaps: 6  
US-10-041-030-4 (1-420) x US-09-925-065A-679103 (1-1345)  
Qy 170 GluLySlaLaAlaLysTrpLyBabnProLpGlyHisMetAspGlyLeuThrThrAspGly 189  
Db 354 GacGGAGGGCCAAATGGGACCCAGATGactCTGAGGAGTGAGCACCACCACTGAA 413  
Qy 190 ValLeuValMetHisProArgGlyGlyPheThrGluSerLysProGlyValTrpArg 209  
Db 414 GTCCTGGTGTGATGCCCGCAGGGGGCTCTCCGAGGACTCACCCCGGGCTCTGGGG 473  
Qy 210 GluLeSerValCysGlyAspValTyrThrLeuArgLysGluSerAlaGlnGlnGlnArg 229  
Db 474 GAGATCTGGTCAGTCGGGAGATGTCACATGCCGGACAGCGCTAGCCAGACGG 533  
Qy 230 GlyLysLeuValGlusLeuGluSerGluThrAsnValLeuGlnAspGlySerLeuLeuLeuCys 249  
Db 534 GccAAAGCAGTA 545  
Qy 250 GlyAlaThrLeuLeuTrpArgThrAlaAspGlyLeuPheHisThrProGlyLysHis 269  
Db 546 --GGTGGCCGCCATC-CCCAC-- 568  
; SEQ ID NO: 38950  
; LENGTH: 3078  
; TYPE: DNA  
; ORGANISM: Bovine 19866880741510  
; US-10-750-185-38950  
Alignment Scores:  
Pred. No.: 34.4 Length: 3078  
Score: 102.00 Matches: 88  
Percent Similarity: 34.3% Conservative: 52  
Best Local Similarity: 21.6% Mismatches: 160  
Query Match: 4.5% Indels: 108  
DB: 8 Gaps: 20  
US-10-041-030-4 (1-420) x US-10-750-185-38950 (1-3078)  
Qy 113 AsnLySgluProValLysTyrGlyGluLeuValValLeuGlyTyrAsnGlyAlaLeuPro 32  
Db 1471 AACAGGGG-----GAGGGCTCATGTTCCAAGGAGGGAAATTCTCATC 1515  
Qy 33 AspGlyAsp--ArgGlyArgArgLysSer-----ArgPheAlaLeuTyrLys 47  
Db 1516 TTAGGAGACTCTAGAGACTTGAGAGAGAGCCCTTCCTGGTAGATTTATTCCT 1575  
Qy 48 ArgProGlyAlaLysGlyLysProSerThrValHisValLeuSerThrProGlnAla 67  
Db 1576 AGACCTTGAGCTCTCCGAGTAAAGAACACTTGTAGCGATTCACCTTGCTCAT 1635  
Qy 68 SerLysAlaLeuSerCysLysGlyGluLysSerIleSerTyrThrLeuSerArgAsnGln 87  
Db 1636 GAAAGACTTAAAGCTTAAGGAAGAAGTGG----GCTCTGTCATGAGAT 1686  
Qy 88 ThrValValValGluTyrThrHisAspLysAspThrAspMetPhe---GlnValGlyArg 106  
; SEQ ID NO: 38950  
; LENGTH: 3078  
; TYPE: DNA  
; ORGANISM: Bovine 19866880741510  
; US-10-750-185-38950  
Alignment Scores:  
Pred. No.: 56.9 Length: 569  
Score: 151.00 Matches: 151  
Percent Similarity: 56.9% Conservative: 151  
Best Local Similarity: 49.0% Mismatches: 151  
Query Match: 5.0% Indels: 151  
DB: 151 GAGGGGTCTCTAGCATAGCTAGGCCTCTG 569  
Qy 288 LeuAsnThrLeuAlaPheProSerIleAsnGlyLysGluValValGluGluLysGlnPro 307  
Db 625 ATCTCCAGCCCTCTGCCCCACAGGCTTCAATCAGGAACTCCAGGCC 684  
Qy 308 TrpAlaTyrLeuSerCysGlyLysValHisGlyTyrHisAsnTrpGlyHisArgSerTAP 327  
Db 685 CAGGGGTCTCTAGCATAGCTAGGCCTCTG-----TCCACAGACAGG- 725  
Qy 328 ThrlGluLiaAsnGluArgGluCysPrometCysArgPheValGlyPro----- 343  
Db 726 AGACAGACAGGCTCCCCAACGATAGCTGCTACACCTGGAGGTCCAGGGGTGATGCG 785  
Qy 344 -----TyrValProLeuTripleu---GlyCys 351  
Db 786 ATCAAGGACACAGACACAGACATACTGTGCTGAGGCTGCTCAAGSGCTGC 836  
RESULT 5  
US-10-750-185-38950  
; Sequence 38950, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMJ GENOMICS, INC.  
; APPLICANT: DENISE SUE K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFIELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; CURRENT APPLICATION NUMBER: US/10/750, 185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US/10/750, 185  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PATENTIN version 3.1  
; SEQ ID NO: 38950  
; LENGTH: 3078  
; TYPE: DNA  
; ORGANISM: Bovine 19866880741510  
; US-10-750-185-38950  
Alignment Scores:  
Pred. No.: 34.4 Length: 3078  
Score: 102.00 Matches: 88  
Percent Similarity: 34.3% Conservative: 52  
Best Local Similarity: 21.6% Mismatches: 160  
Query Match: 4.5% Indels: 108  
DB: 8 Gaps: 20

APPLICANT: KERR, Richard  
 APPLICANT: ROSENFIELD, David  
 APPLICANT: HOLM, Tom  
 APPLICANT: BATES, Stephen  
 APPLICANT: FANTIN, Dennis  
 TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
 FILE REFERENCE: MM1100-1  
 CURRENT APPLICATION NUMBER: US/10/750,623  
 CURRENT FILING DATE: 2003-12-31  
 PRIOR APPLICATION NUMBER: US 60/437,482  
 PRIOR FILING DATE: 2003-12-31  
 NUMBER OF SEQ ID NOS: 64922  
 SOFTWARE: PatentIN version 3.1  
 SEQ ID NO: 38950  
 LENGTH: 3078  
 TYPE: DNA  
 ORGANISM: Bovine 19866880741510  
 US-10-750-623-38950  
 Alignment Scores:  
 Pred. No.: 34.4 Length: 3078  
 Score: 102.00 Matches: 88  
 Percent Similarity: 34.3% Conservative: 52  
 Best Local Similarity: 21.6% Mismatches: 150  
 Query Match: 4.5% Deletions: 108  
 DB: 8 Gaps: 20  
 US-10-041-030-4 (1-420) x US-10-750-623-38950 (1-3078)  
 QY 13 AspArgGlyProValIysTyrGlyGluLeuValValLeuGlyTyrArgGlyValAlaLeuPro 32  
 QY 1471 AACAGGGG.....GACCGCTCATGTTCCAAAGCAGGGATTTCATC 1515  
 QY 33 AspGlyAsp.....ArgGlyArgArgGlySer.....ArgPheAlaLeuTyrIys 47  
 DB 1516 TTAGGAGCTCAGACTTGAGAGGCCCTTCCTGGAGATTTCTCTCTCT 1575  
 QY 48 ArgProLySAlaArgGlyValIysProSerTyrValIysValSerThrProgInala 67  
 DB 1576 AGACCTCACGCTCTCCAGTTAAAGAACAGCTTCAGCTGATTCACCTGTCTCAT 1635  
 QY 68 SerIysAlaSerCysGlyGlnHisSerIysSerTyrThrLeuSerArgArgIn 87  
 DB 1636 GAAAAGACTTAAGCCCTAGGAGAAAGTCG.....GCTCTCTCATGAGAT 1686  
 QY 88 ThrValValValGluTyrThrHisAspIysAspIysAspThrAspMetPhe--GlnValGlyArg 106  
 DB 1747 TCACTCCCTTCCTTGATTT.....ACACTGCCTGAGTCAGTACATTTCT 1800  
 QY 1677 GCAGGTCTATAAGCTTCTTAAGTCCACTGCCTCTAGGAGCTGAGCTGAGA 1746  
 DB 177 Asp.....GluAlaGlnIleThrGlnSerThrKilSerArgPhe 139  
 QY 1801 GAATGTGTCAGTTTCAAATGAAAGAATGACTACACAAACATAATAACT 1860  
 DB 140 AlaCysArgIleValCysAspArgAspGlyProTyrThrAlaArgIlePheAlaIys 159  
 DB 1861 CCATTTCG.....GAAGAACTTCCTCAACAGCTTCAACAGCTTCTCCCTGT 1911  
 QY 160 PheAspSerSerIys.....AsnIlePheLeuGlyGluLeuAlaIysTyr 175  
 DB 1912 ACCATACATTCACAAAGCAGTAACTTACACAGCTTACACAGCTTCAACAGCTAATAGT 1968  
 QY 176 LysAlaProAspGlyIysMetAspGlyIleThrThrArgIysVal.....LeuValMetIhs 194  
 DB 1969 AGAAATTGTAGGG.....AAAGACATAAACACTGAAATGAGTACCTTTACAGAA 2025  
 QY 195 ProArgGlyGlyPhethGluGlySerIys.....ProGlyValTyrArgGlyIleSer 212  
 DB 2026 AACATCTCAACATTCACAGCTTACAGGCTTAAATGTCGAGTGTGAGCTAATAGT 2085  
 RESULT 6  
 US-10-750-623-38950  
 Sequence 38950, Application US/10750623  
 Publication No. US20050287531A1  
 GENERAL INFORMATION:  
 APPLICANT: MMI GENOMICS, INC.  
 APPLICANT: DENISE, Sue K.





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Db 1030 CTGTATGACTCTGGATCAGCGCGTGTG3GACGGCTTGACGCCCTCCC 1089
Qy 282 SglnCypro-----valGlyLeuasnThrLeuAlph 293
Db 1090 TGGTGTGGCGGAAAGCCGGGCTGAGGCGCCCTGAGGCGCTGGCAACAG 1149
Qy 293 eProSerIleAsnArgLysGluValValGluLysGlnProTrpAlaThrLeu 293
Db 1150 TCCCCACCGAGCAGGCCTCTTGTACCCCTAAGCCAGTCACCGAGTC 1201
Qy 313 SglyHisValHisGlyTyrrHisasnTrpGlyHisArgSerIleAspLeu 333
Db 1202 ---CCACCCATCACCGAACCTGG-----GCTAACGCTCC 1236
Qy 333 SglyCyproBrometylCyargThrValGlyProTyrrValProLeuTrpIle 353
Db 1237 CAGGACCCCGTAGGGTGGCGCGAGCTGACTGGCTGGCTGGCG 1293
Qy 353 aGlyPheTyrrValAspAlaGlyProProThrHisAlaPheThrProTyrrVal 373
Db 1294 TGGGTCTCTGACTACTCTGCTCTCAAGCTGTTGAGGAGGCTCCATCAACG 1353
Qy 373 SargLuySserAlaLuyStryrPserGlnIleProLeuProHisGlyTyrrHisAla 393
Db 1354 ACCCCAGCTCCAACTGCTGTCGTCCTCTCCAGCCCTGGCAAGTCAG 1413
Qy 393 ehIsAlaLalaCysProHe-----CysAlaThrClnLeuValGlyGluLnaCys 410
Db 1414 GTGGGGGACCTCAGCCAGCCAGGACAGCTGTTGCTCACTGCGGAAATCAGGGC 1473
Qy 410 Sile 411
Db 1474 AATG 1477

RESULT 10
; Sequence 4, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEAR ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 9913.6000-0000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 164810
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-4

RESULT 11
; Sequence 362, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malando
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 21728
; TYPE: DNA
; ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1)..(21728)
; OTHER INFORMATION: n = A, T, C or G
US-10-330-773-362

Alignment Scores:
US-10-041-030-4 (1-420) x US-11-121-086-4 (1-164810)
Qy 175 TrpLys-AnpProArgLys-HisMetAbpGlyLeuThrThrAsnGlyValLeuValMetH 194
Db 49348 TGGAGCTCAAGGACGGCCACACGTTGGCTTAACAGAGGC----CCACCGC 49295
Qy 194 IsoproArgLysGlyPheThrGluLysSerGlnProGlyValTPargGluLysSerValC 214
Db 49294 ACTGCAAGGGGAC-----GSCAGGTGCAAGGATCCAAGGCT 49256

Alignment Scores:

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Pred. No.: 926 Length: 21728  
Score: 97.00 Matches: 95  
Percent Similarity: 31.6% Conservative: 41  
Best Local Similarity: 22.1% Missmatches: 167  
Query Match: 7 Indels: 128  
Gaps: 21

DB: US-10-041-030-4 (1-420) x US-10-330-773-362 (1-21728)

QY 36 ArgGluArgArgLysSerArgPheAlaLeuThrLysArgProLysAlaAsnDlyVallys 55  
Db 1560 CGGGAGCAGCGAGA-----CGT 1543

QY 56 Pro-Ser-Thr-Val-His-Ser-Ala-Ser-Thr-Pro-Gln-Ala-Ser-Lys-Ala-Ser-Cys-Syl 75  
Db 1542 CCACAGCAGCATCCACAG-----AGGA-----GACGACGCGACATCCACAGGAG 1486

QY 75 YGLNHisSerIleSerTyrrThrLeuSerArgAlaGlnHrValValValGluThrHrHi 95  
Db 1485 ACCACGC-----AGAGTCACAG-----CACAGCAGCATCCACCGAG 1456

QY 95 AspLysAspThrAspMetPheGlnValGlyArgSerThrGluSerProLysAspPheva 115  
Db 1455 CGAGGAGCAGCGAGCAGC-----CACAGCAGCATCCACCGAG 1417

QY 115 IValThrAspThrIleSerGlySerGlnAsnThrAspGluAlaGlnIle----- 131  
Db 1416 GACGACGCGAGAGTCCACAGCAGCACTCCACAGGAGACTGGAGACGAGCAG 1357

QY 132 ---ThrGlnSerThrIleSerArgPheAlaCysAspArgLeuValCysAspArgAsnGluPr 150  
Db 1356 CCACACGAGGAGCAGCAGCAGCTGCCACAGCAGGAGCAGCAGACGAGCTCC 1297

QY 150 GTrYTrHr-----AlaArgLePhe-AlaAlaGlyPheAspSerL 164  
Db 1296 ACAGCACCATCCACAGGAGCTAACGAAATGTCACAGCAGCAGATTCAAGAGGCC 1237

QY 164 YEAaBnIlePheLeuGlyGluLySalaAlaLeuTrpLys-AspProAsp-----GlyHis 181  
Db 1236 CAAAC-----TGGAAACACCAGATGTCCATGACAG 1204

QY 182 MetAspGlyLeuThrThrAsnGlyValLeu-----ValMetHisProArgGly 197  
Db 1203 AAGAGCAGACACAACAAATGTCGCTCTGCACTGCAATGCAATGCTGCTTCAC 1144

QY 198 GLYPheThrGlu---GluserGlnProGlyValTrpArgGluLeSerValCysGlyAsp 216  
Db 1143 GGRATGAACTCTGATACAGCCCTGGAGATGCGCGTGAACAGCCGAGGAGC 1084

QY 217 ValTyrrThrLeuArgGluThrArgSer----- 225  
Db 1083 CAGGAGACATGCATGACATCTGGAGCGCTGGAGTGAGTGGCTGCCAGGCTGG 1024

QY 226 -----AlaGlnDlnArgGlyIleLeuValGluSerGluThrAsnValLeuGlnAspGly 243  
Db 1023 CGAGGAGCAGCGGAGGCGCTGGAGCTGATGGTGCGAGGAGCTCTGGCTGGAGGA 964

QY 244 SerLeutle-----AspLeuCysGlyAlaThrLeuLeuTrpArgThrAlaAspGlyLeu 261  
Db 963 GAGATCTCAAATGATCATCCACAAATTGATCTGGAGAGCAACACCCGA 904

QY 262 PheHisthr-----Pro 265  
Db 903 GCACACACATAACCGGAGCTGGTGGTTGTAATTAGCCCTGAGCTGACCC 844

QY 266 ThrlGlyLysHistileGluAlaLeuArgGlnGluIleLeuAlaAspGlnGlnCysPro 285  
Db 843 ATCTCACCACTGTTGATGCGGTTACCACTGGTC 802

QY 286 ValGlyIleuAsnThrLeuAlaPheProSerIleAsnArgLyGluValValGluGlyLeu 305  
Db 801 ---CTCTAGATGTTCTACTGCTCTCAGGGTCCAGGAGACGCCCTGGCTG 748

QY 306 GlnProTrpAlaTyrieuserCysGlyHisIvalIleGlyTyrHisAlaIPTGlyHisArg 325  
Db 747 GGGGACTGGGGACCTCTAACGIGAATGCTCACACGGT-----GCCTGGGCCAGG 694

QY 326 SerAspThrGluAlaLysGluLysGluCybrometCybargThrValGlyProTyroVal 345  
Db 693 GCCCCCTCAACGAGCTGAGTCAC 656

QY 346 ProLeuTrpLeuGlyCysGlu-----AlaGlyPhe 355  
Db 655 CCCTCAACGAGCTGAGTCACAGGGCCCTGGCTCACAGCATGTTGCGAGGCC 596

QY 356 TyrValAspAlaGlyProProThrHisAlaPheThrProCysGlyHisIvalCysSerGlu 375  
Db 595 CAGCTCACCGGCCACTCCGGAGCTCTGAGCACAGCAGTCGACAC 542

QY 376 LysSerAlaLysTyrTrpSerGlnLeProLeuProHisGlyThrHisAla----- 392  
Db 541 AspGlyCTGCTTATGGCCAGCAGCAGGCCCTGGGCAACACTGGCAGG 482

QY 393 -----PheHisAlaAlaCysPro 398  
Db 481 GGCAGGCTCGGGTAGGCTGGCT 458

DB: RESULT 12  
US-11-112-908-55  
; Sequence 56, Application US/11112908  
; Publication No. US20050260659A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Cole  
; ATTORNEY OR AGENT FOR APPLICANT: Davis, Lisa M.  
; TITLE OF INVENTION: Breast Cancer Biomarker B  
; FILE REFERENCE: 04-164-US  
; CURRENT APPLICATION NUMBER: US/11/112,908  
; PRIOR APPLICATION NUMBER: US 60/564,758  
; PRIOR FILING DATE: 2004-04-23  
; PRIOR APPLICATION NUMBER: US 60/575,978  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US 60/631,702  
; PRIOR FILING DATE: 2005-11-30  
; PRIOR APPLICATION NUMBER: US 60/633,826  
; PRIOR FILING DATE: 2004-12-07  
; NUMBER OF SEQ ID NOS: 511  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 56  
; LENGTH: 150468  
; TPER: DNA  
; ORGANISM: Homo sapiens  
; US-11-112-908-55

Alignment Scores:  
Pred. No.: 8.41e+03 Length: 150468  
Score: 97.00 Matches: 61  
Percent Similarity: 30.2% Conservative: 15  
Best Local Similarity: 24.2% Missmatches: 85  
Query Match: 4.2% Indel: 91  
DB: Gaps: 12

DB: US-10-041-030-4 (1-420) x US-11-112-908-56 (1-150468)

QY 178 ProAspGlyIleMetaspGlyIleThrLeuThrAsnGlyValLeuAlaMethisProArgGly 197  
Db 43500 CGAGACGCCACAGAGCTGGGGAGATCTGGGCTCAGAGCAATTCACAGCGTGA 43559

QY 198 GLYPheThrGluGluSerGlnProGlyValTrpArgGluLeSerValCysGlyArgVal 217  
Db 43560 GTGCGCAAGCTGGAGCTCTGGGGCCCTGGGAGCTCTGGATGAGGT----- 43613

QY 218 TyrThrLeuArgGluThrArgSerAlaGlyLysLeuValGluSerGluThr 237  
Db 43614 -----AGGGGCCGCTGGGAGGGCTGGGG 43643

DB:	12	Gaps:	12
QY	238 AsnValLeuGlnAspGlySerLeuIleAspLeuCysGlyAlaThrLeuLeuTrpArgThr	257	
Db	43644 -----TGCAGGCT-----TGCGGGCT-----	43652	
QY	258 AlaAspGlyLeuPheHisThr--ProThrGlnLySHisIleGluAla-----	272	
Db	43653 GCAGGGCTCTGTGTGTGAAACCCACCGCGCAGACTTCCTCTCGCGATCTAGT	43712	
QY	273 --LeuArgLysGluLileAsnAlaAlaArgProGlnCySProAlaGly	287	
Db	43713 GTCCTCCCTGTATAATGAGGAGCCGCTCAAGTCCCACCCACAGCATGCCAGGG	43772	
QY	288 LeuAlaThrLeuAlaPheProSerIleAsnArgLysGluValValGluGluLysGlnPro	307	
Db	43773 AACCATGGAAAGCATGGATGAGAAAGCAGACGATGTTGGCTCACTCTCGAGAAGTC	43832	
QY	308 -----TGAATAT-----TGAATAT-----	310	
Db	43833 GAGGGGTCTCACATAGGACGCCGGATTGGTCACTCAATGGCAGTAGTCAGCT	43892	
QY	311 -----LeuSerCysGlyHisValHisGlyLysValHisAlaPheProSerIleAsnAla	326	
Db	43893 CTGCTGCCACTCTGCGCCATCTCCAGGTTGGCTCTTGGAGGCACT	43947	
QY	326 rasPthrGluAlaAsnGluArgGluCysProMetCysArgThrValGlyProTyroValPr	346	
Db	43948 -----CCTTTCCTCCCCACAGGGACACGAGCTACTCTCA	43985	
QY	346 oleuTrpLeuGlyCysGluAlaLysGlyPheTyrValAspAlaGlyProProThrHisAlaPh	366	
Db	43986 TGGCTGTGTTGGGTTCCACGCC-----TACCCCTGAGCATCAC	44024	
QY	366 eTerPro---CysGlyHisValCysSerGluLysSerAlaLysTyrTrpSerGlnIlePr	385	
Db	44025 AACGCCAGGGCAGGCCAGTG-----TGGTCCCTCTACCC	44060	
QY	385 oleuProHis-----GlyThrHis 391		
Db	44061 GCTACCCCACTCTGGGTACTTAAGGGTCACAT	44094	
<b>RESULT 13</b>			
US-11-112-908-55			
; Sequence 55, Application US/1112908			
; Publication No. US20050260659A1			
; GENERAL INFORMATION:			
; APPLICANT: Harris, Cole			
; APPLICANT: Davis, Lisa M.			
; TITLE OF INVENTION: Breast Cancer Biomarkers			
; FILE REFERENCE: 04-164-US			
; CURRENT APPLICATION NUMBER: US/11/112,908			
; CURRENT FILING DATE: 2005-04-22			
; PRIOR APPLICATION NUMBER: US 60/564,758			
; PRIOR FILING DATE: 2004-04-23			
; PRIOR APPLICATION NUMBER: US 60/575,978			
; PRIOR FILING DATE: 2004-06-01			
; PRIOR APPLICATION NUMBER: US 60/631,702			
; PRIOR FILING DATE: 2004-11-30			
; PRIOR APPLICATION NUMBER: US 60/633,826			
; PRIOR FILING DATE: 2004-12-07			
; NUMBER OF SEQ ID NOS: 511			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 55			
; LENGTH: 193789			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; US-11-112-908-55			
Alignment Scores:			
Pred. No.:	1.12e+04	Length:	193789
Score:	97.00	Matches:	61
Percent Similarity:	30.2%	Conservative:	15
Best Local Similarity:	24.2%	Mismatches:	85
Query Match:	4.2%	Indels:	91
DB:	12	Gaps:	12
QY	218 TyrThrIleArgGluLysArgSerAlaGlnGlnArgGlyLysValLeuValGluLysGlnPro	237	
Db	93799 -----AGGGGCGCGCTGGGCGGCGCTCGGG-----	93828	
QY	238 AsnValLeuGlnAspGlySerLeuIleAspLeuCysGlyAlaThrLeuTrpArgThr	257	
Db	93829 -----TGCAGGCT-----	93837	
QY	258 AlaAspGlyLeuPheHisThr--ProThrGlnLySHisIleGluAla-----	272	
Db	93838 CTGAGGCTCTGTGTTGAAACCCACCGCTGCGGAGCTCGGATCTGAGTCAGT	93897	
QY	273 -----LeuArgLysGluLysValHisGlyLysValHisAlaPheProSerIleAsnAla	287	
Db	93898 GTCCTCTCTGTGAAATGGAGAACGCCACCTGCGGAGCTCTCCCTCAGGATCTGAG	93957	
QY	288 LeuAlaThrLeuAlaPheProSerIleAsnArgLysGluValValGluGluLysGlnPro	307	
Db	93958 AACATGCGGCTCACATTAGGACACGCCGGTTGGTCACTCAATGGCACTAAGTCAGT	94017	
QY	311 -----LeuSerCysGlyHisValHisGlyLysValHisAlaPheProSerIleAsnAla	326	
Db	94018 GAGGGGTCTCACATTAGGACACGCCGGTTGGTCACTCAATGGCACTAAGTCAGT	94077	
QY	326 rasPthrGluAlaAsnGluArgGluCysProMetCysArgThrValGlyProTyroValPr	346	
Db	94133 -----CCTTTCCTCCCCACAGGGACACGGAGCTACTCTCA	94170	
QY	346 oleuTrpLeuGlyCysGluAlaLysGlyPheTyrValAspAlaGlyProProThrHisAlaPh	366	
Db	94171 TGGCTGTGTTGGGCTCCGGCC-----TACCCCTGAGCACATCAC	94209	
QY	366 eTerPro---CysGlyHisValCysSerGluLysSerAlaLysTyrTrpSerGlnIlePr	385	
Db	94210 AACGCCAGGGCAGGCCAGTG-----TGGTCCCTCTACCC	94245	
QY	385 oleuProHis-----GlyThrHis 391		
Db	94216 GCTACCCCACTCTGGGTACTTAAGGGTCACAT	94279	
<b>RESULT 14</b>			
US-11-112-908-55			
; Sequence 41, Application US/11183136			
; Publication No. US2006001989611			
; GENERAL INFORMATION:			
; APPLICANT: Li, Dean			
; TITLE OF INVENTION: NETRIN-RELATED COMPOSITIONS AND USES			
; FILE REFERENCE: UUTH-P01-011			
; CURRENT APPLICATION NUMBER: US/11/183,136			
; PRIOR APPLICATION NUMBER: US 60/587,796			
; PRIOR FILING DATE: 2004-07-14			
; NUMBER OF SEQ ID NOS: 44			
; SOFTWARE: FastSEQ for Windows Version 4.0			
; SEQ ID NO 41			
; LENGTH: 1770			

; TYPE: DNA  
; ORGANISM: Mouse  
US-11-183-136-41

Alignment Scores:  
Pred. No.: 59 Length: 1770  
Score: 96.50 Matches: 92  
Percent Similarity: 33.2% Conservative: 38  
Best Local Similarity: 23.5% Mismatches: 140  
Query Match: 4.2% Indels: 122  
DB: 1.2% Gaps: 21

US-10-041-030-4 (1-420) x US-11-183-136-41 (1-1770)

Qy 36 ArgLyArgArgLysSerArgPheAlaLeuTyrLysArgProLysAlaLysGlyValLys 55  
Db 291 CAGGGAACTATGAGGAGCTTGCTACTACTGGCAAGCT 329

Qy 56 ProSerThrValHisSerValLeSerThrProGlnAlaSerLysAlaLysSerCysLysGly 75  
Db 330 -----CAGTCGAGCTACACCCAG-----TCACTAGAGGC 362

Qy 76 GluHis-SerIleSerTyrThrLeuSerArgAsnGlnThr-----ValValValGluThr 93  
Db 363 CAACATCACCTCTCATGGACAGAGGCTGAGTTGACAGACACGCTGTGACTTT 422

Qy 93 RTRHISAspLysAspThrAspMet-----PheDlnValGlyArgSerThr 108  
Db 423 TGTAGTATGCCGCCAGGTATGAGCTCTGAGAAGTCCCAGACATGGCGC---AC 479

Qy 108 RGLUserProLeaRspPheValAlaValThrAspThrLeSer-----GlySerGlnAsnThr 126  
Db 480 CTGGCAGCCCTACCACTGCTTACAGCTTGAGAGACTGATGGGCCATCTGCCG 539

Qy 126 rasPglLalAGlnIleRglsrThrLeSerArgAspAlaCysArgIleValCysAs 146  
Db 540 ACCTGCCGAGAACATGTCACCTTCAGGCCAACGGGGTCTGC----- 585

Qy 146 PArGAsnLysLysProTyrThrAlaArgIlePheAlaAlaLysGlyAspSerSerLysAsnI 166  
Db 586 ---ACCGAGGACTACTCACGC-----TGGCAAGGTCAAGAGAGAGAGAGATGT 632

Qy 166 e-----PhelUgLyGluLysAlaLalaLysTrpLysAsnProAsp--GlyHisMetAs 183  
Db 633 GCCTTGTAGGTAGGACGCCGCTTGCCATCTTGCCGCCCTGACCTGGPACATOGA 692

Qy 183 PsylLeuThrIleAspGlyValLeuValMetHisProArgArgLysGlyPheThrGluSe 203  
Db 693 CAACTGTGACAGAGG-----ATGGAG 716

Qy 203 RGNProGlyValTrpArgGluIleSerValCysGlyAspValTyrThrLeuArgLys 223  
Db 717 CGCCAAGGGCTC-----AAGAGTCCTCACTTACTGACT 755

Qy 223 rArgSerAlaGlnGlnArg-----GlyLysLeuValGluSerGlnThr----- 237  
Db 756 GCGCATGCCCTGCGCTGGCTGGGACCTACGCGAGGAGAACTTA 815

Qy 238 -----AsnValLeuGlnAspGlySerLeuIleAspIleCys-GlyAlaThrIle 254  
Db 816 CAAGTACTCTATGCCATCTCCMATATGAGGATCTGGCTGAGCTGGCGAC 875

Qy 254 eutPArgThrAlaAspGlyLeuPheHiSThrProThrGlnLysHistoleGluAlaLeu 274  
Db 876 TG-----CCAACCTGTGACAGGCGGAG----- 898

Qy 274 rggLngLysLeuAlaAlaArgProGlnCysProValGlyLeuAsnThrLeuAlaPhePhe 294  
Db 899 -----AspGAGCTGAGCTGAGGAGCTGACACA----- 928

Qy 294 roserileAsnArgLysGluValGluGluLysGlyProTrpAlaPheSerCysG 314  
Db 929 -----ACACCAAGGCCCGAGCTGGCG 953

Qy 314 LysValHisGlyTyRhiAsnTrpGlyHiSerAspThrGluAlaLysGluArgG 334  
Db 954 GT-----GCAAGAGAATCTCCCCACACGGCCTGGCGC 989

Qy 334 IucysPrometCysArg-----ThrValGlyProTyrValPro 346  
Db 990 TGGCTCCATCTGCGGCCACGGCTCTCCAAATGCCATGCGCTGGCGC 1049

Qy 347 LeuTrpIleGlyCysGluAlaGlyPheTyrValAspAlaGlyProProThrHisAlaPhe 366  
Db 1050 CTTGGGCTGAGGAGGACCTACTAT-----GCCGCTTGCGGAGACGCTC 1100

Qy 367 Thr-ProCysGlyLysValHisGlySerGluLysSerAlaLysTyrTrpSerGlnIleProLeu 386  
Db 1101 CTCCTGGGCCACGGGCTCTCCAGTGGAGAACTGTAGCTACTCTGCTGCGTCCTC 1160

Qy 387 Pro--HisGlyThrValAlaPheHisAla 395  
Db 1161 CCAGGCCAGGACTCTAGCTTTCGACT 1190

RESULT 15

US-10-750-185-32846

; Sequence 32846; Application US/10750185  
; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MM GENOMICS, INC.

; APPLICANT: DENISE SUE K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENBLUM, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM11100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: PatentIN version 3.1

; SEQ ID NO 32846

; LENGTH: 1363

; TYPE: DNA

; ORGANISM: Bovine 19866880713026

US-10-750-185-32846

Alignment Scores:  
Pred. No.: 67.1 Length: 1363  
Score: 94.50 Matches: 58  
Percent Similarity: 35.0% Conservative: 28  
Best Local Similarity: 23.6% Mismatches: 78  
Query Match: 4.1% Indels: 83  
DB: 8 Gaps: 13

US-10-041-030-4 (1-420) x US-10-750-185-32846 (1-1363)

Qy 205 ProGlyValTrpArgGlu----- 210

Db 27 CGGGCCCTGGAGGAGGACCTGGCTCTCGAGATCTCCAGGGAGCTTGGCGAC 86

Qy 211 -----IleSerValCysGlyAspValTyrThrLeuArgLysHistoleGluAlaLeu 227

Db 87 CACGGCTCTCCAGCTGCGCTGGCTGGCGCTGGCGCTGGCGCTCCCGCC 146

Qy 228 GluArgGlyLysLeuValGlySerGluThrAlaValLeuGlnAspLysSerIleLeuAsp 247

Db 147 TCCAGACCACCTCAAGGGCCCGCTGGCGCTCCAGGCA 204

Qy 248 LeuCysGlyValAlaLeuLeuTrpArgThrAlaAspGlyLeuPheHiSThrProThrGln 267

Db 205 TrIGC----- 210

Qy 268 LysHistidineGluAlaLeuArgGlnGluIleAsnAlaAlaArgProGlnCysProValGly 287  
 Db 211 ---CACCCGAGCACCCTGCTTCACTTCAGCTCGCCAGCAGTCTGCCAGTGGCTGGAGTGGT 267  
 Qy 288 LeuAsnThrLeuAlaLpheProSerIleAsnArgGluVal---ValGluIleGlu--- 305  
 Db 268 GTC----GTAATGTTACCCATTTCAGACAAGAACAGCACTGGCTCAGAGAGGGCA 321  
 Qy 306 -----GlnProTP---AlaTyroLeuSerCysGlyIleValHis 317  
 Db 322 ATGACTGGTCGAGGGCTCGCCGCACTGGGAGGAGCAGCTGAATCA-----AAC 372  
 Qy 318 GlyTyRHisAsnTrpGly---HisArgSerAspPheGluAlaArgGluArgGlyCysPro 336  
 Db 373 TCTGACTCTACTCTGGCCCGGACTCTGACGTCACGCCTCTCAAGGAGGACTC 432  
 Qy 337 MetCYBargThrValGlyProTyRValProLeuIlePheGlyCysGluAlaGlyPhe--- 355  
 Db 433 AGCIGCTAGAAATCTCAAATCTAC-----TGTGAGGAGGTGTGC 474  
 Qy 356 -----TyrValAspAlaGlyProPro-----Thr 363  
 Db 475 AGAGCCCTGCTGTTCCATCTATCTCTCTGACCAACCTGAGAAGGCTTGAGAAG 534  
 Qy 364 HisAlaPheThrProCysGlyIleValCysSerGlu----- 375  
 Db 535 CACAGGGAGCCCTCCGCTGGCTGCTGCTGAGCTCTCTGCGCGCTCTCTC 594  
 Qy 376 -----LysSerAlaLysValIlePheProLeuProHisGlyThrHis---Ala 392  
 Db 595 CTCTGGGGTCCCAGAACCCAGCAAGCTCCCGGCTCTGGTACCCACTGAGCC 654  
 Qy 393 PheHisIalaAlaCysPro 398  
 Db 655 CAGCACAGGCCAGGCC 672

Search completed: March 2, 2006, 07:44:06  
Job time : 1418 secs

GenCore version 5.1.7  
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Om protein - nucleic search, using frame\_plus\_p2n model  
 Run on: March 2, 2006, 06:06:38 ; Search time 1066 Seconds  
 (without alignments)  
 3258.104 Million cell updates/sec

Title: US-10-041-030-4  
 Perfect score: 2290

Sequence: 1 MFSPGQEHCAPNPKPVKG.....ATOLVGEONCNIKLFQGPID 420

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
 Ygapop 10.0 , Ygapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delext 7.0

Searched: 9793542 seqb, 413468905 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODE=frame+pn, model -DEV=xlh  
 -Q=/abes/ABSSWEB spool/US10041030/runat 01032006 134411 21967/app\_query.fasta\_1  
 -MATRIX=blosum62 -TRANS=human40\_cdi -LIST=45 -DOCALIGN=100 -THR SCORE=pct  
 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MOD=LOCAL -OUTRPT=pfo -NORM=eect  
 -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes05in  
 -USER=US10041030 @CGN 1.1 1026 @runat 01032006 134411 21967 -NCPU=6 -1CPU=3  
 -NO MAR -NGC SCORES=0 -WRIT=0 -LOGLOG -DEV TIMEOUT=120  
 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=0 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DELEXT=7

Database : Published Applications\_NA\_Main.\*

1: /cgn2\_6/ptodata/1/pubpna/hs07\_PUBCOMB.seq:\*

2: /cgn2\_6/ptodata/1/pubpna/hs08\_PUBCOMB.seq:\*

3: /cgn2\_6/ptodata/1/pubpna/hs09A\_PUBCOMB.seq:\*

4: /cgn2\_6/ptodata/1/pubpna/hs09B\_PUBCOMB.seq:\*

5: /cgn2\_6/ptodata/1/pubpna/us10A\_PUBCOMB.seq:\*

6: /cgn2\_6/ptodata/1/pubpna/us10B\_PUBCOMB.seq:\*

7: /cgn2\_6/ptodata/1/pubpna/us10C\_PUBCOMB.seq:\*

8: /cgn2\_6/ptodata/1/pubpna/us10D\_PUBCOMB.seq:\*

9: /cgn2\_6/ptodata/1/pubpna/us10E\_PUBCOMB.seq:\*

10: /cgn2\_6/ptodata/1/pubpna/us11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### RESULT 1

US-10-085-117-288

; Sequence 288, Application US/10085117

; GENERAL INFORMATION:

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

; FILE REFERENCE: 52945200421

; CURRENT APPLICATION NUMBER: US/10-085,117

; CURRENT FILING DATE: 2002-02-27

; PRIORITY APPLICATION NUMBER: US 09/798,586

; NUMBER OF SEQ ID NOS: 361

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 288

; LENGTH: 1263

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-10-085-117-288

; Alignment Scores:

; Pred. No.: 8.2e-255

; Score: 2290.00

; Percent Similarity: 100.0%

; Best Local Similarity: 100.0%

; Query Match: 100.0%

; DB: 6

; Gaps: 0

	Sequence 5, Appli
Score:	Sequence 5, Appli
Percent Similarity:	Sequence 5, Appli
Best Local Similarity:	Sequence 5, Appli
Query Match:	Sequence 5, Appli
DB:	Sequence 5, Appli
Gaps:	Sequence 5, Appli

QY 1 MetPheSerProGlyGlnGluGluIleCysAlaProAsnGluProValIleValTyrIle 20  
 Db 1 ArgTrtTccCtcGccAGGAGAACTGGCCCAATAGAACGCCAGTGAAATACGG 60  
 QY 21 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProArgIlyAspArgIlyArgIly 40  
 Db 61 GAGCTGGGTGCTGGGTTACATGGTTTACCAATGGAGTAGGGAGGAGGAA 120  
 QY 41 SerArgPheAlaLeuTyrIleValTyrAsnGlyAlaLeuProAsnGlyAspArgIly 60  
 Db 121 AGTAGATTGCCCCTACAGCGCCCAAGGCAATGGTCMAACCCAGCACCGTCAT 180  
 QY 61 ValLeuSerThrProGlnAlaSerLysAlaIleSerCysLeuGlyCysIleSerIle 80  
 Db 181 GTGATATCCACGCCAGCATCCAAAGCTATCGTCAAACTGCAACAGTATCC 240  
 QY 81 TyrThrLeuSerArgAsnGlnThrValValGluIlePheGlnGlyProLeAsp 100  
 Db 241 TACCTTCTTCAGGATCAGACTGGTGGAGTACACATGATTAAGATGGATCAT 300  
 QY 101 MetPheGlnValGlyArgSerTyrIleValTyrAsnProIleAspPheValIle 100  
 Db 301 ArgTTCAGGTGGCAGATCACAGAAAGCCATATCGACTTGTGTCAACACAGT 360  
 QY 121 SerGlySerGlnAlaThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
 Db 361 TCTGGCAGGAGACAGACGAGCCAGATCACAGAGCACATTCAGCTGTCGC 420  
 QY 141 CysArgIleValCysAspArgAspGluProTyrThrIlaArgIlePheAlaAlaGlyPhe 160  
 Db 421 TGCAGGATGCTGGGACGAACTTACAGCAGGATTCGCCCGGATT 480  
 QY 161 AspSerSerIleAsnIlePheLeuGlyGluIleAlaIleAspIleAsnProAspIle 180  
 Db 481 GACTCTCCAAACATAATTCTTGAGAAAGCAGCAAGTGAAACCCGACGGC 540  
 QY 181 HisMetAspGlyIleThrIleThrAlaGlyValLeuValMetIleProArgIlyGlyPheIle 200  
 Db 541 CACATGGATGCGCTACTACTAATGGCGCTCTGGTGTGATCATCCACGAGGCTTCAC 600  
 QY 201 GluGluSerGlnProGlyValTyrArgGluIleSerValCysGlyAspValIleValTyrIle 220  
 Db 601 GaggAGtCCAGCCGGGAGTCGGCGAGATCTCTGCTGGAGAGCTGTCACCTG 660  
 QY 221 ArgGluIleArgSerAlaGlyGlnIleLeuGluSerGluThrAlaValIle 240  
 Db 661 CGAGAAACCCAGGCGCCAGCAGCAGGAGCTGGTGAAGTGTCTG 720  
 QY 241 GluAspGlySerIleIleAspLeuCysGlyAlaThrLeuLeuIleArgThrAlaAspIle 260  
 Db 721 CAGCAGGCTCCCTCATGGACTCTGCTGGCCACTCTCTCTGGAGACAGCTG 780  
 QY 261 LeuPheHisThrProIleGlnIleBisIleGluAlaLeuArgGlnGluIleAlaAla 280  
 Db 781 CTTTTCTACTTCACTGAGGAGACATAGACCCCTGGGAGGAGTTAACCC 840  
 QY 281 ArgProGlnCysProValGlyLeuAsnThrLeuIlePheProSerIleAsnArgIlyGlu 300  
 Db 841 CGGCTCACTGCTCTGGGGCTAACACCTGGCCATCTCTGGAGACGGTACCA 900  
 QY 301 ValValGluGluIleGlyIleLeuProArgIlyLeuAsnGlyAlaLeuProAsnGlyAspMetCysArgThr 320  
 Db 901 GTCGTTGGAGGAGAAGCAGCCCTGGCATATCTCTGGAGACGGTACCA 960  
 QY 321 AsnTrpGlyHisSerAspThrGluAlaAsnGluGlyCysProMetCysArgThr 340  
 Db 961 AACGGGGCCATCGAGGAGCAGGAGGAGGAGTCCATGTCAGGACT 1020  
 QY 341 ValGlyProTyrValProLeuLeuIleGlyGluIleGlyIlePheTyValAspAlaGly 360  
 Db 1021 GTGGGCCCTATGTCCTCTGGCTGCTGGAGGAGATTTGTAACGCGAGA 1080  
 QY 361 ProProThrHisAlaPheThrProCysGlyIleValCysSerGlyIleSerAlaLysTyr 380

---

RESULT 2  
 US-10-197-666A-135  
 ; Sequence 135, Application US/10197666A  
 ; Publication No. US20030092037A1  
 ; GENERAL INFORMATION  
 ; APPLICANT: ASAMI KASEI KABUSIKI KAISHA  
 ; TITLE OF INVENTION: Phosphorylation related gene  
 ; FILE REFERENCE: PH-1548US  
 ; CURRENT APPLICATION NUMBER: US/10/197-666A  
 ; PRIORITY FILING DATE: 2002-11-18  
 ; PRIORITY APPLICATION NUMBER: JP 2001-218204  
 ; PRIORITY FILING DATE: 2001-07-18  
 ; PRIORITY APPLICATION NUMBER: JP 2001-263450  
 ; PRIORITY FILING DATE: 2001-08-31  
 ; PRIORITY APPLICATION NUMBER: JP 2002-012176  
 ; PRIORITY FILING DATE: 2002-01-21  
 ; PRIORITY APPLICATION NUMBER: US 6/0/305,884  
 ; PRIORITY FILING DATE: 2001-07-18  
 ; PRIORITY APPLICATION NUMBER: US 6/0/316,304  
 ; PRIORITY FILING DATE: 2001-09-04  
 ; PRIORITY APPLICATION NUMBER: US 6/0/350,027  
 ; PRIORITY FILING DATE: 2003-01-23  
 ; NUMBER OF SEQ ID NOS: 156  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 135  
 ; LENGTH: 5579  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (177)..(1436)  
 ; US-10-197-666A-135

Alignment Scores:  
 Pred. No.: 6.8e-254 Length: 5579  
 Score: 2490.00 Matches: 420  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 5 Gaps: 0

US-10-041-030-4 (1-420) x US-10-197-666A-135 (1-5579)

QY 1 MetPheSerProGlyGlnGluGluIleCysAlaProAsnGluProValIleValTyrIle 20  
 Db 177 ArgTrtTccCtcGccAGGAGAACTGGCCCAATAGAACGCCAGTGAAATACGG 236  
 QY 21 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProAsnGlyAspArgIlyArgIly 40  
 Db 237 GACTGGGTGCTGCTGGAGTACATGGCTTACCCATGGGATGAGGAGGAGAA 296  
 QY 41 SerArgPheAlaLeuTyrIleValTyrAsnGlyAlaLeuProAsnGlyAspArgIly 60  
 Db 297 ATGAGATTGCCCCTACAGCGCCAGGAGCAATGGTCACACAGTCAT 356  
 QY 61 ValLeuSerThrProGlnAlaSerLysAlaIleSerCysGlyIleSerIleSer 80  
 Db 357 GTGATTCACGCCAGCATCCAAAGCTATCAGCTGCAAGGTCAACAGTATCC 416  
 QY 81 TyrThrLeuSerArgAsnGlnThrValValGluIlePheGlnIleAspAspIle 100  
 Db 417 TACACTTGTCTGGGAGTCACTGCTGGGGAGGAGTACACCATGATAGGATACGGAT 476

FILE REFERENCE: 529452000121

CURRENT APPLICATION NUMBER: US10/085,117

CURRENT FILING DATE: 2002-02-27

PRIORITY FILING DATE: 2001-03-02

NUMBER OF SEQ ID NOS: 361

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 287

LENGTH: 5597

TYPE: DNA

ORGANISM: Homo sapiens

US-10-085-117-287

Qy 101 MetPheGlnValGlyArgSerThrGluSerProLeuPheValValThrAspThrile 120  
 Db 477 ArgTTTCAGTGCGCAGATCACAGAAAGCCATTCGACTTCCTGTGCAACAGATT 536

Qy 121 SerGlySerGlnLanthAspGluAspGluAspGluAspGluAspGluAspGluAsp 140  
 Db 537 TCTGGCAAGCCAGAACGAGGAGGCGAGTACACAGAGCACCATTCGGTGC 596

Qy 141 CyBargIleValCysAspArgAspGluProTrpThrAlaArgLysSerGlyAsp 160  
 Db 597 TCGAGGATGGTGGTGGGACGAGGATGAACTTACAGACGACGATATGCCCGGATT 656

Qy 161 AspSerSerLysAsnIlePheLeuGlyValGluValAlaAlaAlaAlaAlaAla 180  
 Db 657 GACTCTTCAAACATATTCCTTGAGGAAGAACGCAAGTGAAAGACCCGACGCC 716

Qy 181 HisMetAspGlyIleuthThrAspGlyValLeuValMetHisIleAspGlyIlePhe 200  
 Db 717 CACATGGATGGCTGACTACTAATGGCCCTCTGGATGATTCACAGACGATATGCCCGATT 776

Qy 201 GluGluSerGlnProGlyValLeuTrpArgGluLeuSerValCysGlyAspValTyr 220  
 Db 777 GAGGAGTCCAGCCGGGAGGCTTGCGGAGAGCTCTGCTGCTGAGATGTCACCTG 836

Qy 221 ArgGluLysArgSerIleGlyValGluGlyValLeuValGluSerGluThrValLeu 240  
 Db 837 CGAGAAACCGAGCTGGCCAGAGCAAGAACGCAAGTGAAAGCTGGCTG 896

Qy 241 GluAspGlySerIleuLeuAspIleValCysGlyValAspIleLeuLeuLeuLeu 260  
 Db 897 CAGGAGCCTCCATGACTCTGCTCTGGCCACTCTCTCTGGAGACACGAGATGG 956

Qy 261 LeuPheIstIleProTrpGlnLysHistidineGluAlaLeuArgGlnGluLeuAla 280  
 Db 956 CAGGAGCCTCCATGACTCTGCTCTGGCCACTCTCTGGAGACACGAGATGG

Qy 281 AspProGlnCysProValGlyValGluAspLeuProSerIleAspTyrGlyVal 300  
 Db 1017 CGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1076

Qy 301 ValValGluGlyIleGluProTrpAlaIleSerGluGlyValAspGlyValAsp 320  
 Db 1077 GCTGGGAGGAGGAGGACCCCTGGCATATCTGGCTGGCCAGTCACCGTACCTAC 1136

Qy 321 AsnTrpGlyIleAspSerAspGluGluGlyValGluGlyCysProMetCysArgThr 340  
 Db 1137 ACTGGCCCTATGCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1196

Qy 341 ValGlyProTrpValProLeuProTrpGluGluGlyCysGluGlyIlePheTrpAla 360  
 Db 1197 GTGGCCCTCTGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1256

Qy 361 ProProTrpIleIleIlePheThrProCysGlyIleValIleSerGluIleSerAla 380  
 Db 1257 CCGCCAACTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 1316

Qy 381 TrpSerGlnIleProLeuProIleGlyIleGlyIleAlaAlaCysProPhenylCys 400  
 Db 1317 TGGCTCAATCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1376

Qy 401 AspGlyGluGlyValGluGlyAspGlyIleValLeuLeuPheGlyProLeuAsp 420  
 Db 1377 GCTACACAGCTGGTGGGAGGAACTGCTCAATTAATTTCAGGTCCTATGAC 1436

RESULT 3  
 US-10-085-117-287  
 ; sequence 287, Application US/10085117  
 ; Publication No. US20030233341  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris, David W.  
 ; APPLICANT: Engelhard, Eric K.  
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

Db 897 CAGGACGCTCCCTCATGGACTCTGGGCACTCTCTGGAGAACASCGATGG 956 Qy 1 MetPheSerProArgLysGluLysCysAlaProAlaLysGluLysProAlaLysTyrGly 20  
 Qy 261 LeuPheHisThrProArgLysLysIleGluLalaLeuArgIngluLeuAlaAla 280 Db 501 ARGTTTCCCAGCCAGGAGAACCTGCSCCCCAATAAGGAGCCAGTAACGG 560  
 Db 957 CTTTCTACTCCAACTGAGCACATAGAACGCCCTCGGGAGGATTAACGCC 1016 Qy 21 GluLeuValValLeuIgLyTyraAngIYAlaLeuProAlaLysAspArgLysArgLys 40  
 Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlaPheProSerIleAsnArgLysGlu 300 Db 561 GAGCTGGGGGCTGGAGCTACATGGCTTCACCCATGGAGATGGAGGAGAA 620  
 Qy 1017 CGGCTCTAGTGCTGTGGAGCCACACCTGGCTCCAGCATCAACAGAAGAG 1076 Qy 41 SerArgPheAlaLeuIysArgProIysAlaAsnLysValIysProSerLysProSerLys 60  
 Db 301 ValValGluGluLysGlnProTrpAlaTyLeuSerCysGlyHisIvalHisGlyTyrHis 320 Db 621 AGTAGATTGCCCCCTACAGGGCCAAAGGCAATGGTCAACCGACGGTCACT 680  
 Qy 1077 GAGCTGGGGGAGGAGCAGCCCTGGCAGATCTCAGTTCGGGCACTGGCAAGGGTACAC 1136 Qy 61 ValIleSerThrProGlnAlaSerIysAlaIleSerCysLysValGlyGlnHisSerIleSer 80  
 Qy 321 AsnTrpGlyHisArgSerAspThrGluLalaAsnGluArgGluCysProMetCysArgThr 340 Db 681 GTCGATTCACGCCCGAGCAATGGCTACAGTCAGCAGTCAGATTC 740  
 Db 1137 ACTGGGGCCATCGAGTCACGGAGGCAACGAGGGCTGCCCAGTGAGGACT 1196 Qy 81 TyThrIleSerArgArgGlnThrValValGluTyrrHisAspLysAspTrp 100  
 Db 1257 CCCCAACTCATGACTCTCCCTGGACACGCTGCTGAGA 1316 Qy 741 IACACTTGTCAGGATCAGCTGTTGGGAGGATCACACATAATAAGATAGGAT 800  
 Db 1197 GTGGGCCCTATGCTCTCTGCTTCTGCTGAGGAGGATTTATGAGCCAGGA 1256 Qy 101 MetPheGlnValGlyArgSerThrGluSerProLeuPheValThrAspThrIle 120  
 Qy 361 ProProThrHisAlaPheThrProCysGlyHisValCysSerGluLysSerAlaLysTyr 380 Db 801 AIGTTGGGGGAGTCATGCTATGCCATGCTGCTGCTGCTTCTG 860  
 Db 381 TrpSerGlnIleProLeuProHisGlyThrHisAlaPheAlaLysCysProPheCys 400 Qy 121 SerGlySerGlnAlaSerIysAlaIleSerCysLysValGlyGlnHisSerIleSer 140  
 Db 1317 TGGCTCTAGATCCCGTGTGCTCATGGAACTCATTCGTTCACTGCTGCTGCTGCTG 1376 Db 861 TCTGGCAACGAGCACAGCAAGGCAATGGCTATGCCATGCTGCTGCTG 920  
 Qy 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleLeuIlePheGlyProLeuP 420 Qy 141 CyBargIleValCysAdargArgAlaGluProThrAlaArgLeuAlaLysPhe 160  
 Db 1377 GCTACACAGCTGGTGGGGAGACAATCTCAATTATTTCAGTCCATTGAC 1436 Db 921 TGGAGGATGCTGGGAGGAGGATGAACTTACAGCAGCAATTTGGAAAGGCAACAGTGGAA 980  
 Qy 161 AspSerSlysAsnIlePheLeuGlyGluLysAlaAlaLysTrpLysAsnProArgPhe 180 Db 981 GACTCTCCAAAACATTTCTGGAGAAAGGCAACAGTGGAA 1040  
 Result 4  
 US-10-041-030-3  
 ; Sequence 3: Application US/10041030  
 ; Publication No. US20020150934A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Powers, Scott  
 ; APPLICANT: Mu, David  
 ; APPLICANT: Xiang, Phil  
 ; APPLICANT: Peng, Yue  
 ; APPLICANT: Tularik Inc.  
 ; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian  
 ; TITLE OF INVENTION: Pellino Polypeptides and Polynucleotides  
 ; FILE REFERENCE: 016781-006810US  
 ; CURRENT APPLICATION NUMBER: US/10/041.030  
 ; CURRENT FILING DATE: 2001-12-28  
 ; PRIOR APPLICATION NUMBER: US 60/259,502  
 ; PRIOR FILING DATE: 2001-01-02  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 5921  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1501)..(1763)  
 ; OTHER INFORMATION: human pellino 2  
 ; US-10-041-030-3  
 Alignment Scores:  
 Pred. No.: 7.4e-254 Length: 5921  
 Score: 2290.00 Matches: 420  
 Percent Similarity: 100 % Conservative: 0  
 Best Local Similarity: 100 % Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 5 Gaps: 0  
 US-10-041-030-4 (1-420) x US-10-041-030-3 (1-5921)

Qy 1 MetPheSerProArgLysGluLysCysAlaProAlaLysGluLysProAlaLysTyrGly 20  
 Db 501 ARGTTTCCCAGCCAGGAGAACCTGCSCCCCAATAAGGAGCCAGTAACGG 560  
 Db 957 CTTTCTACTCCAACTGAGCACATAGAACGCCCTCGGGAGGATTAACGCC 1016  
 Qy 21 GluLeuValValLeuIgLyTyraAngIYAlaLeuProAlaLysAspArgLysArgLys 40  
 Db 561 GAGCTGGGGGCTGGAGCTACATGGCTTCACCCATGGAGATGGAGGAGAA 620  
 Qy 41 SerArgPheAlaLeuIysArgProIysAlaAsnLysValIysProSerLysProSerLys 60  
 Db 621 AGTAGATTGCCCCCTACAGGGCCAAAGGCAATGGTCAACCGACGGTCACT 680  
 Qy 61 ValIleSerThrProGlnAlaSerIysAlaIleSerCysLysValGlyGlnHisSerIleSer 80  
 Db 681 GTCGATTCACGCCCGAGCAATGGCTACAGTCAGCAGTCAGATTC 740  
 Qy 81 TyThrIleSerArgArgGlnThrValValGluTyrrHisAspLysAspTrp 100  
 Db 741 IACACTTGTCAGGATCAGCTGTTGGGAGGATCACACATAATAAGATAGGAT 800  
 Qy 101 MetPheGlnValGlyArgSerThrGluSerProLeuPheValThrAspThrIle 120  
 Db 801 AIGTTGGGGGAGTCATGCTATGCCATGCTGCTGCTGCTG 860  
 Qy 121 SerGlySerGlnAlaSerIysAlaIleSerCysLysValGlyGlnHisSerIleSer 140  
 Db 861 TCTGGCAACGAGCACAGCAAGGCAATGGCTATGCCATGCTGCTG 920  
 Qy 141 CyBargIleValCysAdargArgAlaGluProThrAlaArgLeuAlaLysPhe 160  
 Db 921 TGGAGGATGCTGGGAGGAGGATGAACTTACAGCAGCAATTTGGAAAGGCAACAGTGGAA 980  
 Qy 161 AspSerSlysAsnIlePheLeuGlyGluLysAlaAlaLysTrpLysAsnProArgPhe 180  
 Db 981 GACTCTCCAAAACATTTCTGGAGAAAGGCAACAGTGGAA 1040  
 Qy 181 HisMetArgPheLeutyrThrIgLyValLeuAlaMetHisProArgLysGlyPheThr 200  
 Db 1041 CACATGGATGGGCTCACTACTATGGCTCCCTGGTGAATGCACTCAGGGCTTCAC 1100  
 Qy 201 GluGluLysSerGlnProGlyValTrpArgGluIleSerValCysGlyAspValTyrrIle 220  
 Db 1101 GAGGAGTCACCCGGGGCTCGGGGAGTCCTCTGGAGATGTGAGATGTGAGACACTTG 1160  
 Qy 221 ArgGluLysSerAlaAlaGlnIgLyValLeuValGluSerGluLysSerAlaAla 240  
 Db 1161 CGAGAACGAGCTCCCTCATGGCTGCCAGCACAGGAAAGCTGGAGAATGCAACACGCTTG 1220  
 Qy 241 GluArgPheSerIleAspIleCysGlyIaLysLeuValGluSerGluLysSerAlaAla 260  
 Db 1221 CAGGAGCTCCCTCATGGCTGCCAGCACAGGAAAGCTGGAGAATGCAACACGCTTG 1280  
 Qy 261 LeuPheHisThrProTrpGlnIysHisIleGluLalaLeuArgGlnGluIleLeuAla 280  
 Db 1281 CTTTCTACTCCAACTGAGCACATAGAACGCCCTCCGGAGGATTAACGG 1340  
 Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlaPheProSerIleAsnArgLysGlu 300  
 Db 1341 CGGCTCTAGTCCTGGGGTCACCCCTGGCTCCGGAGATCAACGGAGA 1400  
 Qy 301 ValValGluGluLysGlnProTrpAlaTyLeuSerCysGlyHisIvalHisGlyTyrHis 320  
 Db 1401 GAGCTGGGGGCTGGAGCTACAGTCAGTTCGGCCACGCGACGGTACAC 1460  
 Qy 321 AsnTrpGlyHisArgSerAspThrGluLalaAsnGluArgGluCysProMetCysArgThr 340  
 Db 1461 AACCTGGGGCCATGGAGGAGCAGGCCAACGAGGGAGTGCCCATGTCAG 1520  
 Qy 341 ValIgLyProTrpAlaProLeuTrpLeuIgLyCysGluLalaLysPheThrValAspAlaLys 360  
 Db 1521 GTGGGCCCTATGCTCTCTGGCTGTGGCTGAGGAGGTTTGTAGAGCAGCGAGA 1580  
 Qy 351 ProProThrHisAlaPheThrProCysGlyHisIvalCysSerGluLysSerAlaLysTyr 380

RESULT 5  
US-09-843-905A-7

; Sequence 7, Application US/09843905A  
; Publication No. US20020168683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Cosman, David J.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-A  
; CURRENT FILING DATE: 2001-04-27  
; CURRENT APPLICATION NUMBER: US/09/843, 905A  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 7  
; LENGTH: 1263  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-843-905A-7

Alignment Scores:

Preド. No.:	5.32e-254	Length:	1263
Score:	283.00	Matches:	419
Percent Similarity:	99.8%	Conservative:	0
Best Local Similarity:	99.8%	Mismatches:	1
Query Match:	99.7%	Indels:	0
DB:	3	Gaps:	0

US-10-041-030-4 (1-420) x US-09-843-905A-7 (1-1263)

QY 1 MetPheSerProGlyGlnGluGluIleCysAlaProAlaLysGluProValValGly 20  
Db 1 ArgTrpTCCCTGGCCAGGAGAACTCGGCCCAATAAGAGCCGTGAAATCGG 60  
QY 21 GluLeuValValLeuGlyTyrArgLysValLeuProAsnGlyAspArgGly 40  
Db 61 GAGCTGGGGCTGGCTGGGGCTACAGATGGCTTACCCATGGAGTAGGGAGGAA 120  
QY 41 SerArgPheAlaLeuTyrIleArgProLySAlaLysProSerThrValHis 60  
Db 121 AGTAGATTTGCCCTACAGGGGCCAGGGAATGGTGAAACCCGCCGTCAT 180  
QY 61 ValIleSerThrProGlnAlaSerLysAlaIleSerCysLysGlnIleSer 80  
Db 181 GGTGATTCACGCCGCCAGGCATCCAGCTCAAGTCACAGTATTC 240  
QY 81 Tyr-ThrLeuSerArgAspGlnLeuValValGluIleArgSerIleAspThrAsp 100  
Db 241 TACCATTTGTCAGGAATCACGCTGGTGGAGTACACATGAAAGTACATT 300  
QY 101 MetPheGlnValGlyArgSerThrGluSerProIleAspPheValValThrAspThrIle 120  
Db 301 ATGTTTCAAGTGGCGAGATCAACGAAAGCCATATGACTTGTGACACACATT 360  
QY 121 SerGlySerGlnAlaSerLysAlaGlnIleSerGlnIleSerIleSerGlnIleSer 140  
Db 361 TCTGGCAACGAAACGAGCAAGCCGAGCAACGAGCCAAATCCGGTGGC 420  
QY 141 CysArgIleValCysAspArgAsnGluProTyRThrIleArgIlePheAlaAlaLys 160  
Db 421 TGGAGGATCGTGTGGCAAGGAGATGAACTTACAGCACGAGATATTCGCCCCGGATT 480

RESULT 6  
US-10-317-250-7

; Sequence 7, Application US/10317250  
; Publication No. US20030165945A1  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Cosman, David J.  
; APPLICANT: Li, Xiaoxia  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-B  
; CURRENT APPLICATION NUMBER: US/10/317,250  
; CURRENT FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 7  
; LENGTH: 1263  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-317-250-7

QY 161 AspSerSerLysAsnIlePhenGlyGluIleAlaAlaLysProAlaProAla 180  
Db 481 GACTCTTCACAAACATATTCCTGGAGTAAGGCAGCAGTGGAAGAACCCGAGGC 540  
QY 181 HisMetAspGlyLeuThrThrArgIleValMetIleProArgGlyGlyPhethr 200  
Db 541 CACATGGATGGCTACTACTAAATGGCTCGGATGCTCCATCCAGGAGGGCTTACCC 600  
QY 201 GluLysSerGlnProGlyValTrpArgGlyIleSerValCysGlyAspValTyRthrIle 220  
Db 601 GAGGATGCCACCGGGGCTGGCCGAGATCTCTGCTGGAGATGTTACCTG 660  
QY 221 ArgGluIleArgSerAlaGlnGlnIleArgGlyIleLeuValGluSerGluIleAspVal 240  
Db 661 CGAGAACCCAGCTGGCCACAGGAGAGCTGGAGAGTCAGCAACGTCCTG 720  
QY 241 GluAsnGlySerLeuIleAspLeuCysGlyAlaIleLeuTrpGlnAlaArgPhe 260  
Db 721 CAGGAGGCTCCCTCATGAGCTGCTGCTGGGGCTCAGCTCCAGATCAACGAGATGG 780  
QY 261 LeuPheIleIleProThrGlyIleGluIleLeuIleLeuIleLeuTrpGlnAlaArgPhe 280  
Db 781 CTTTCTGATACCCACTCAGGAGCTAGAAGCCATAGAGCCATAGAGCC 840  
QY 281 ArgProGlnCysProValGlyLeuIleThrIleAlaPheProSerIleAspArgIleGlu 300  
Db 841 CGCCCTAGTGCTCTGGGGCTCAGCTCCAGATCAACGAGATGGAGAG 900  
QY 301 ValValGluGluIleGlnProTrpAlaTyRleuSerCysGlyIleValHisGlyIleThrIle 320  
Db 901 GGGTGGAGGAGAGCAGGCCCTGGGACATATCTAGCTGTTGGCCACCTGCTGG 960  
QY 321 AsnTrpGlyIleSargSerAspThrGluIalAsnGluIleArgGlyProMetCysArgThr 340  
Db 961 AACTGAGCCATGGAGTGAAGTGACAGGAGCCACAGGAGGAGTGCCAGTGAGG 1020  
QY 341 ValGlyProTyRValProLeuTrpLeuGlyCysGluIalGlyPhetTyRValAspAlaGly 360  
Db 1021 GGGGCCCTATGGCTCTGGCTGCTGGAGGGAGATTATGAGGGAGGA 1080  
QY 361 ProProThrHisAlaIleIleProCysGlyIleValCysSerGlnIleAspAlaLysTrp 380  
Db 1081 CGGCCAACTCAGTCCTTCACTCCCTGAGACAGCTGCTGGAGAGTCAGTCAAAATAC 1140  
QY 381 TrpSerGlnIleProLeuProIleGlyIleGluIleAlaIleAlaCysProPhes 400  
Db 1141 TCTCTGAACTCCGTTGCTCTGCTGCTGAGGATTTGAGGGAGGA 1200  
QY 401 AlaIleGlnLeuValGlyGluGlnAlaCysIleValIlePhenGlyProIleAsp 420  
Db 1201 GCTACAGCTGCTGGAGGAAACTGCACTCAAAATTTCGAAAGGTCATGAC 1260

## Alignment Scores:

Pred. No.: 5.32e-254 Length: 1263  
 Percent Similarity: 99.8% Matches: 419  
 Best Local Similarity: 99.8% Conservative: 0  
 Query Match: 99.7% Mismatches: 1  
 DB: 6 Indels: 0 Gaps: 0

US-10-041-030-4 (1-420) x US-10-317-250-7 (1-1263)

QY 1 MetPheSerProGlyGlnGluGluHisCysAlaProAsnLysGluProValThrValTyrGly 20  
 1 ATGTTTCCTCTGCCAGGAGAACACTCGCCGCCAAATAGAGGCCAGTAGAAATACGG 60  
 21 GluLeuValValLeuUglyTyrAsnGlyAlaLeuProAsnGlyAspArgLysArgLys 40  
 61 GAGCTGGTGTCTGGGTACATGTGCTTACCCAAATGGAGATAGAGGAGGAGGAGA 120  
 41 SerArgPheAlaLeuTyrLysAspProLysAlaAsnGlyValLysProSerThrValHis 60  
 121 ATGAGATTGCCCTACAGGCCCAAGGAAATGGGTCAAACCCAGCACCGTCT 180

QY 61 ValLeuSerThrProGlnAlaSerLysAlaSerCysLysGlyGlnHisSerIleSer 80  
 181 GTGATATCCAGGCCAGGAGCATCCAGGCTTAAGCTGCAAGGTCACACGATATCC 240  
 81 TyrThrLeuSerArgArgGlnThrValValValGluThrHisAspLysAspThrAsp 100  
 241 TACACTTGTCAGGATCAGTCTGGTGTGGAGTAGACATGATAAGATAGGAT 300

QY 101 MetPheGlnValGlyArgSerThrAlaSerProIleAspPheValValThrAspThrIle 120  
 301 ATGTTTCAGGTGGCAGATCACAGAAAGCCTAACGACTCTGTTGTCAGACAGAT 360

QY 121 SerGlySerGlnAsnThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
 361 TCTGCAGCCAGCACGAGGAGGCCAGATCACAGAGCACATACAGGAGCCATTCCTCCC 420  
 141 CysArgIleValCysAspArgAspGluIleProTyrThrAlaArgIlePheAlaIleGlyPhe 160

QY 421 TGCAAGATCTGTGGAGACAGGAATCACACGAGCATTCGCCGGGATT 480

QY 161 AspSerSerLysAsnLeuHeleUglyGluValAlaAlaLysTryptAsnProAspGly 180  
 481 GACTCTTCCAAACATATTTCTTGAGTAAAGCAGCAAGTGGAAGAACCCGACGC 540

QY 181 HisMetAspGlyLeuThrThrAspGlyValLeuValMetHisProArgGlyGlyPheThr 200  
 541 CACATGGAGGGCTCACTACTAAATGGGCTCTGGTATGCCACAGAGGGGCTTCCC 600

Db 201 GluGluSerIleInProGlyValTrpArgGluIleSerValCysGlyAspValThrIle 220  
 601 GAGGAGTCCCAGCCGGGGTCTGGCCGAGATCTCTGTCGTGGAGATGTGACCTG 660

QY 221 ArgGluThrArgSerAlaGlnGlnArgGlyLysLeuValGluSerGluThrAspValLeu 240  
 661 CGAGAAACCKAGTCGCCCCAGCAAGGAGAAAGCTGTCGTGGAGATGTGACCTG 720

QY 241 GluAspGlySerLeuLeuAspLeuCysGlyValThrLeuLeuTrpArgThrAlaAspGly 260  
 721 CAGAACGGCTCCCTCATTAAGCTCTGGTGTGGAGAACCTCTCTGGAGACAGCAGATGG 780

QY 221 ArgGluThrArgSerAlaGlnGlyLysLeuValGluSerGluThrAspValLeu 240  
 661 LeuPheIleThrProThrGlyIleHisIleGluAlaLeuUglyGluLeuAspAlaAla 280  
 781 CTTTTCATCACTCCCACTCAAGGACATAGAGCCTCGGCAGGAGATTAGCCGCC 840

QY 281 ArgProGlyCysProValGlyLeuAspThrLeuAlaPhoProSerIleAsnArgLysGlu 300  
 841 CGGCTCTAGCTCTCTGGCTCACACCTGGCCCTCCAGCATCACAGGAG 900

QY 301 ValValGluIleUglySerInProTrpAlaThrLeuSerCysGlyLysValHisGlyTyrHis 320  
 901 GTGGGAGGAGGAAGCAGCCCTGGCCATACTCAGTTGGGCCACGTGACGGSTACAC 960

QY 321 AsnTRPGLYHisArgSerAspThrGluAlaEnglurGluGlySPrometCysArgThr 340  
 951 AACGGGCCATGGAGGACACGGAGGCCACAGGAGCTGCCCACGACT 1020

Db 341 ValGlyProTryValProLeuTrpLeuLysProGlyCysGluAlaGlyPheThrValAspAlaGly 360

Db 1021 GTGGCCCTATGCTCTCTGGCTGTGGAGTTAGACGCCAGGA 1080

QY 351 ProProThrHisAlaPheThrProCysGlyAlaValCysSerGluLysSerAlaValTyr 380  
 1081 CCGCCAATCTCATGCTTCACTCCTGAGACGCTGCTGAGTCTGCAAAATAC 1140

QY 381 TRPSerGlnIleProLeuProHisGlyThrHisAlaAlaLysProHeCys 400  
 1141 TGCCTCGATCCGTCCTCATGGACTCATGCAATTGCTCTGCTGCTGCTCTG 1200

Db 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleLeuIlePheGlnGlyProleAsp 420  
 1201 GCTACACAGCTGGTGGGAGCAAACTGCATCAAAATTAAATTCCAGGTCAATGAC 1260

RESULT 7  
 US-10-258-703-7  
 ; Sequence 7, Application US/10258703  
 ; Publication No. US20040034199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; ATTORNEY: Cosman, David J.  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; CURRENT APPLICATION NUMBER: US/10/258,703  
 ; CURRENT FILING DATE: 2002-10-24  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1263  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-258-703-7

Alignment Scores:

Pred. No.: 5.32e-254 Length: 1263  
 Percent Similarity: 99.8% Matches: 419  
 Best Local Similarity: 99.8% Conservative: 0  
 Query Match: 99.7% Mismatches: 1  
 DB: 7 Indels: 0 Gaps: 0

US-10-041-030-4 (1-420) x US-10-258-703-7 (1-1263)

QY 1 MetPheSerProGlyGlnGluGluHisCysAlaProAsnLysGluProValThrValTyrGly 20  
 1 ATGTTTCCTCTGCCAGGAGAACACTCGCCGCCAAATGGGCAAGGCTGTGAAATACGG 60  
 21 GluLeuValValLeuUglyTyrAsnGlyAlaLeuProAsnGlyAspArgLysArgLys 40  
 61 GAGCTGGTGTGCTGCCAGGAGAACCTCTTACCTCATGGAGATGTGACCTG 120

QY 41 SerArgPheAlaLeuTyrLysAspProLysAlaAsnGlyValLysProSerThrValHis 60  
 121 ACTAGATATGGCTCTAACAGGCCAGGAAATGGTCAAACCCAGCACGGTCAAT 180

QY 61 ValLeuSerThrProGlnAlaSerLysAlaIleSerCysLysGlyGlnHisSerIleSer 80  
 181 GTGATATCCAGGCCAGGAGAACCTCTGCTCAAGGCTCAACAGGTCAAACAGTATCC 240

QY 81 TyrThrLeuSerArgArgGlnIleProValValGluThrHisAspLysAspThrAsp 100  
 241 TACACTTGTCAGGATCAGCTGTCGTGGAGATGTGACATGAAAGGATACGAT 300

QY 101 MetPheGlnValGlyArgSerThrGluSerProIleAspPheValValThrAspThrIle 120  
 301 ATGTTTCAGGTGGCAGATCAACAGAAGGCCPATCGTCACTCTGGTGTGACACGAGATT 360



Db 778 CTTTCAGCTCTACTCAGAACATAGAACCCCTCGCAGGAGTCAATGCAGC 837  
Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlpheProSerIleAsnArgLysGlu 300  
Db 839 CAGCCCCAAGCTGGCCGCTGAGCTTACACCTTGCCCTTCCCAGCATACCGAGAA 897  
Qy 301 ValValGluGluGluGlnProTrpAlaThrLeuSerCysGlyHiSValHiSGLYTHis 320  
Db 898 GTGGTGGAG 957  
Qy 321 AsnTrpGlyHiSArgSerAspThrGluAlaAsnGluArgGluCysProMetCysBargThr 340  
Db ::::: 1018 GTGGGGCCCTACGRCCTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1077  
Qy 958 ArgTrpGlyHiSArgSerAspThrGluAlaAsnGluArgGluCysProMetCysBargThr 1017  
Qy 341 ValGlyProTrpValProLeuTrpLeuGlyCysGluAlaGlyPheTrpValAspAlaGly 360  
Db 1138 TGGTGGGAGATCCACTGCCCAGGAACGGCTGCTGAGGAGATTTATGCGAGGA 1137  
Qy 381 TrpSerGlnIleProLeuProHiSGLYTHisAlpheHiSAlaAlaCysProHeCys 400  
Db 401 AlaThrGlnLeuValGlyLeuGlyAsnCysValLeuPheGlnGlyProLeuAsp 420  
Db 1198 GCCAGCGCACTGGTGGTCAACAGACTCATAATTGTTCCAGGTCCAGTGAC 1257  
**RESULT 9**  
US-10-317-250-5  
; Sequence 5: Application US/10317250  
; Publication No: US20030105945A1  
; GENERAL INFORMATION:  
; APPLICANT: BIRD, Timothy A.  
; APPLICANT: Li, Xiaoxia  
; APPLICANT: Bird, Timothy A.  
; FILE REFERENCE: 2990-B  
; CURRENT APPLICATION NUMBER: US/10/317,250  
; CURRENT FILING DATE: 2002-12-11  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1260  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; US-10-317-250-5  
Alignment Scores:  
pred. No.: 1 1566-241 Length: 1260  
Score: 215.50 Matches: 399  
Percent Similarity: 95.0% Conservative: 10  
Best Local Similarity: 95.0% Mismatches: 10  
Query Match: 6 Indels: 1  
Gaps: 1  
US-10-041-030-4 (1-420) x US-10-317-250-5 (1-1260)  
Qy 1 MetPheSerProGlyGluGluHiSArgSerAspLeuProValAspAlaGlyPheTrpValAspAlaGly 20  
Db 1 ATGTTTCGCCGGCCAGGAGGAACCCAGCCGGCTTACAGGAGCTTAACGG 60  
Qy 21 GluLeuValValLeuGlyTyrAspGlyAlaLeuProAspGlyAspArgGlyArgGly 40  
Db 61 GAGCTGGTGGCTCCGGGCTTACAGGGCTTACCTAATGGTCAAGGGAGGAGAA 120  
Qy 41 SerArgPhoAlaLeuValGlyAspProLySAlaAsnGlyValAspSerTrpValHis 60  
Db 121 AGCAGATTGCCCTATAGGGACACTACGCCAGTGGCTAACATGTTCCAGGTCCAGTGAC 180  
61 ValLeuSerThrProGlnAlaSerLysAlaLeuSerCysLysGlyGlnHiSSerIleSer 80  
Db 181 ATGGTCTCACACCAACAGGGGTCAGCCATCAGCAGCATCACAGCATCG 240  
Qy 81 TyrThrIleSerArgAspGlnThrValValGlyTrpThrIleAspPheTrpIle 100  
Db 241 TACAGTGTGTCAGGAGCCAGGGTGTGGTGGAGTACACCGTT 300  
Qy 101 MetPheGlnValGlyArgSerThrGluSerProLeuAspPheValValThrAspThrIle 120  
Db 301 ArgTrpGlyHiSArgSerAspGluAlaGlyIleThrIleSerThrIleSerArgPheAla 140  
Qy 121 SerGlySerGlnAlaSerAspGluAlaGlyIleThrIleSerThrIleSerArgPheAla 140  
Db 361 TCCGGCTCTGAGGAGAT--GCCAGATCACAGGACCCATGCTGCTGCA 417  
Qy 141 CysArgIleValCysAspArgAspGluProTrpThrAlaArgLePheAlaAlaGlyPhe 160  
Db 418 TSGAGGAGCTGTTGAGGAGCAAGGAGCCTATACGACGATATTGCGSCAGGATTC 477  
Qy 161 ArgSerSerLysAsnIlePheLeuGlyGluIleValAlaValAspTrpLysAsnProAlaGly 180  
Db 478 GATCTCTCAAAATACTTCTCTGAGGAGAGGACCAATGAAAACCTGTGGA 537  
Qy 181 HisMetArgPheGlyLeuThrThrArgLysValLeuValMetHisProArgGlyIlePheThr 200  
Db 538 CACATGGTAGGACTCATHACCACCATGGTCTCTAGTGAACCCGAGGAGCTCACC 597  
Qy 201 GluGluSerGlnProGlyValTrpArgGluIleSerValCysGlyAspValTrpThrLeu 220  
Db 558 GAGGAATCCACGCTGGCTGAGGAGACGATCTCTCTCTCTGGGAGTGTGACCTTG 657  
Qy 221 ArgGlutArgArgSerAlaGlnGlnArgGlyLysLeuValGluSerGluThrAsnValLeu 240  
Db 658 CGAGAGCAGGCTGGCCAGGAGGGAAGCTGCTGGAAAGCTGACCCACGGCTTG 717  
Qy 241 GluAspGlySerLeuIleAspLeuPheCysGlyAlaThrLeuLeuPheArgThrAlaAspGly 260  
Db 718 CAGAGCCGCTCCCTCATGGACTCTGGGGCACTCTCTCTGGAGAACCCGAGATGGC 777  
Qy 251 LeuPheHiSAspProTrpGlnLysHiSAlaLeuGluAlaAspGlyLysLeuAspValTrpLeu 280  
Db 778 CTTTCAGCTCTACTCAGAACATAGAACCCCTCGCAGGAGTCAATGCAGC 837  
Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlpheProSerIleAsnArgLysGlu 300  
Db 839 CGACCCCTGCTGCCCTGGCCCTAACCCCTGGCTTCCCGATCAACGGAGAA 897  
Qy 301 ValValGluGluGluGlnProTrpAlaThrLeuSerCysGlyHiSValHiSGLYTHis 320  
Db 898 GTGGTGGAG 957  
Qy 321 AsnTrpGlyHiSArgSerAspThrGluAlaAsnGluArgGluCysProMetCysBargThr 340  
Db 958 AGCTGGGGCCATCGAGGAGACGCCAGAACCCAGGAGGGAGCTCCATGCGACT 1017  
Qy 341 ValGlyProTrpValProLeuTrpLeuGlyCysGluAlaGlyPheTrpValAspAlaGly 360  
Db 1018 GGGGGCCCTACCTCCCTCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1077  
Qy 351 ProProTrpHiSAlaPheThrProCysGlyHiSValCysSerGluLysSerAlaLeuAsp 380  
Db 1078 CCCCAACTCACCTTCACTCCCTCTGGGGAGCTCTGCTGCAAAAGCTGCGCAACT 1137  
Qy 381 TrpSerGlnIleProLeuProHiSGLYTHisAlpheHiSAlaAlaCysProHeCys 400  
Db 1138 TGGTGGGAGATCCACTGCCCTGGAGAGCAGCGTTCTAGCCGCTGGCTGG 1197  
Qy 401 AlaThrGlnLeuValGlyGluGlyAsnCysValLeuPheGlnGlyProLeuAsp 420  
Db 1198 GCCAGCGAGCTGTTGGAGAGAAGCTGCTAACATGTTCCAGGTCCAGTGAC 1257  
**RESULT 10**  
US-10-085-117-285

Sequence 285, Application US/1008511  
 Publication No. US20030232334A1  
 GENERAL INFORMATION:  
 APPLICANT: Morris, David W.  
 INVENTOR: Engelhard, Eric K.  
 TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
 FILE REFERENCE: 528452000121  
 CURRENT APPLICATION NUMBER: US/10/085,117  
 CURRENT FILING DATE: 2002-03-27  
 PRIORITY APPLICATION NUMBER: US 09/798,586  
 NUMBER OF SEQ ID NOS: 361  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 285  
 LENGTH: 1260  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-10-085-117-285

Alignment Scores:  
 Pred. No.: 1.56e-241 Length: 1260  
 Score: 2175.50 Matches: 399  
 Percent Similarity: 97.4% Conservative: 10  
 Best Local Similarity: 95.0% Mismatches: 10  
 Query Match: 95.0% Indels: 1  
 DB: 6 Gaps: 1

1 MetPheSerProGlyGlnGluGluHisCysAlaProAlaLysGluProValLeuTyrGly 20  
 1 ATGTTTCCCGGAACTGGAGAACCCACGCCCAACAAAGGGCTCGTGAATACGG 60  
 21 GluLeuValValLeuLeuGlyTyrArgLysAlaLeuProArgLysValAspArgLys 40  
 61 GAGCTGAGGTCTGGGAGTACAGTGGCTTACCTTAATGGTCACAAAGGGAGGAA 120  
 41 SerArgPheAlaLeuTyrLysArgProLysAlaAsnGlyValLeuProSerThrValHis 60  
 121 ASCGAGATTCGCCTCTATAAGCGGACTAACGGCAGTGGTGTCAAACCGCACATCAC 180  
 61 ValIleSerThrProGlnAlaSerLysAlaLysSerCysLysGlyLysIleSer 80  
 181 ATGGCTCCACACCAACGGCTCAAGGCCATCGTCAGAGCATCAGCATTCAG 240  
 81 TyrThreUserSerArgAlaGlnThrValValValGluThrIleSAspDysPheAsp 100  
 241 TACAGCTGTCAGGAGCCAGGGTACTGGTGGAGTACACAGATAAGCACGAC 300  
 101 MetPheGlnValGlyArgSerThrGluSerProLeuPheValValIleThrAspThrIle 120  
 301 ATGTTTCCGGGGCAGGTCAACAGAAAGGCCATTGACTTCGTGGTCACAGACCTT 360  
 121 SerGlySerGlnAlaThrAspGluAlaIleThrGlnSerThrIleSerArgPheAla 140  
 361 TCCGGCGCTCAGAACGAGAT--GCCAGATCACACAGACCACTCTAGTGCA 417  
 141 CysArgIleValCysSerPheArgAspGluProThrAlaArgTlePheAlaAlaLysPhe 160  
 201 GluGluSerGlnProGlyValTgargGluLeuSerValCysGlyAlaPheValThrIle 220  
 598 GAGGAAATCCAGCTGGACTCTGAGGAGGAGATCTCTGTCGAGGGATGTTGACCTTG 657

US-10-041-030-4 (1-420) x US-10-085-117-285 (1-1260)

1 MetPheSerProGlyGlnGluGluHisCysAlaProAlaLysGluProValLeuTyrGly 20  
 1 ATGTTTCCCGGAACTGGAGAACCCACGCCCAACAAAGGGCTCGTGAATACGG 60  
 301 ValValGluGlyLysGlnProProAlaTyrLeuSerCysGlyLysValHisLysTyrHis 320  
 898 GTCGCCCCAGTGCCCGTGGCTTAACCCCTGGCTTCCCAGCATCACACGGAGAA 897  
 281 ArgProGlyCysProValGlyLeuAsnThrLeuAlaPheProSerIleAsnArgLysGlu 300  
 718 CAGACGCTCTCTCATGACCTGTCGGGGCCACTCTCTGGTGAACGACCGAGATGC 777  
 241 GluAspGlySerLeuIleAspLeuCysGlyAlaThrLeuLeuPheArgThrAlaAspGly 260  
 261 LeuPheHisThrProThrGlyLysIleGluAlaLeuArgGluGlnGluLeuAlaAla 280  
 778 CTTTTCACTGCTCTACTCTGAGGACATAGAGCCCTCCGAGGAGATCATGGAGCC 837

QY 321 AsnTrpGlyIleArgSerAspThrGluAlaEnglurArgLysProMetCysArgThr 340  
 958 AGCTGGGCCATCGGAGACGCCAAACAGAGGGCTGTCATGTCAGCTCAGACT 1017  
 341 ValGlyProTyroValProLeuIlePheLeuGlyCysGluAlaLysPheTyrValAspAlaLys 360  
 1018 GTCGGCCGCTACTGCTCCCTCCTGAGCTGGAGCTGAGCAGATTGTCGATGCGGA 1077  
 QY 361 ProProThrIleAlaPheThrProCysGlyIleValCysSerGluLeuSerAlaLysTyr 380  
 Db 1078 CCCCAACTCTACGCTTTCACCCCTCGGGCTGGCTGCTGCTGAGAAAGTCCTGCAACTAC 1137  
 QY 381 TrpSerGlnIleProLeuProHisGlyThrIleAlaPheHisAlaAlaCysProPheCys 400  
 Db 1138 TCTCGGAGATCCOACTGCCCAACGGGACGGCAGCGTTCAGCCGCCGCTGCTG 1197  
 QY 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleLeuIlePheGlnLysProLeuAsp 420  
 Db 1198 GCAACGGCAGCTGGTTGGTGAACGAACTGTCATCAAATGATTGTTCCAGGTCCAGTGGAC 1257

RESULT 11  
 US-10-258-703-5  
 ; Sequence 5, Application US/10258703  
 ; Publication No. US20040034199A1  
 GENERAL INFORMATION:  
 APPLICANT: Bird, Timothy A.  
 INVENTOR: Cosman, David J.  
 TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 FILE REFERENCE: 299-US  
 CURRENT APPLICATION NUMBER: US/10/258,703  
 CURRENT FILING DATE: 2002-10-24  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 5  
 LENGTH: 1260  
 TYPE: DNA  
 ORGANISM: Mus musculus  
 US-10-258-703-5

Alignment Scores:  
 Pred. No.: 1.56e-241 Length: 1260  
 Score: 2175.50 Matches: 399  
 Percent Similarity: 97.4% Conservative: 10  
 Best Local Similarity: 95.0% Mismatches: 10  
 Query Match: 95.0% Indels: 1  
 DB: 7 Gaps: 1

US-10-041-030-4 (1-420) x US-10-258-703-5 (1-1260)

QY 1 MetPheSerProGlyGlnGluGluHisCysAlaProAlaLysGluProValLeuTyrGly 20  
 1 ATGTTTCCCGGAACTGGAGAACCCACGCCCAACAAAGGGCTCGTGAATACGG 60

QY 21 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProAsnGlyAspArgLysArgLys 40  
 61 GACCTGGTGTCTCTGGGTACTAGTCTTACTTAATGGTCACGGCGAGGAA 120  
 41 SerArgPheAlaLeuTyrLysArgProlysAlaAsnGlyValIysProSerThrValHis 60  
 121 AGCGATTGCCCTATAGGGACCTACGGCAGGGTGCAACCCGACAGCATCC 180  
 61 ValIleSerThrProGlnAlaSerLysAlaSerCysLysGlyAlaSerIleSer 80  
 QY :::::::::::::::::::::|||||||:|||||||:|||||||:|||||||:|||||||:  
 181 ATGGCTCCACACACAGGGCTCAAGGCCATAGCTCAGCATCACGCATATCG 240  
 QY 81 TyrThrLeuSerArgAsnGlnThrValValAlaGluThrIleSerGlyAspThrPhe 100  
 Db 101 MetPheGlnValGlyArgSerThrGluSerProIleAspPheValValThrAspThrIle 120  
 301 ATGTTTCAAGTGGCAGGCTAACAGAAGCCCTTGAATCTGGTCTGAGACGTT 360  
 121 SerIleSerGlnAlaSerThrIleAspGluLysGlnIleThrGinSerThrIleSerArgPheAla 140  
 Db 361 TCCCGGGTCAGAACGAGAT--GCCAGATCACACAGCACCATCTAGTCGA 417  
 QY 141 CysArgIleValCysAspArgAsnGluProTyrThrIleArgIlePheAlaAlaGlyPhe 160  
 418 TGCAAGATCCTGTTGACAGGAACTACAGACGATTCGGCGCGGATC 477  
 QY 161 AspSerSerIleSambIlePheLeuGlyGluLysAlaLysIleAspAsnProAspGly 180  
 Db 478 GATCTCCAAATATCTTCTTCTGAGAGAACGAAATAGAAACCTGATGGA 537  
 QY 201 GluGluSerGlnProGlyValTpaRgGuIleSerValCysGlyAspValTyrThrIle 220  
 598 GAGGAAATCCCAAGCTTGGAGCTCTGGAGAGATCTCTGCTGCTGGGATCACCCTG 657  
 QY 221 ArgGluLysArgSerAlaGlnGlnArgGlyLysIleValGluSerGluThrAspValIeu 240  
 Db 658 CGAGAGACGGTGGCCGAGCAGGGAAAGTGGCGAAAGTGGCGAAAGCTCTG 717  
 QY 241 GluAspGlySerIleIleAspLeuCysGlyAlaThrLeuIleTpaRgThraIaAspGly 260  
 Db 718 CAGAGCGGTCCCTCATGACTCTGCTGTCGGAGAACGGAGATGCC 777  
 QY 261 LeuLeuIleIleProThrGlnLeuIleIleIleLeuIleLeuIleAla 280  
 Db 778 CTTTTCACGCTCTACTCTGAGGACATGAGGCTCGGGAGGATCAATGCA 837  
 QY 281 ArgProGlnCysProValGlyLeuAsnMileuAlaPheProSerIleIleAspGlyIle 300  
 Db 838 GACCCACGGCCCGTGGACTTAACACCTGACCTTCACCGAAAGAA 897  
 QY 301 ValValGluLysArgInProTrpAlaThrLeuSerCysGlyIleValIleGlyIleIle 320  
 Db 898 GTGGTGGGAAAGCAGCCCTGGGACATACTGAACTGCGGCCATGTGGCACGGCTACAC 957  
 QY 321 AsnTrpGlyIleAsnGlySerIlePheAlaAsnGluAspGluProValLeuPro 340  
 958 :::::::::::::::::::::|||||||:|||||||:|||||||:|||||||:  
 QY 341 ValGlyProTrpValProLeuTrpLeuGlyYsgluAlaGlyPheTyValAspAlaGly 360  
 Db 321 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProAsnGlyAspArgLysArgLys 40  
 QY 278 GACCTGGTGTCTGGGACCTACAGTGGCTTACTTAATGGTCACGGCGAGGAA 337  
 Db 218 ATGTTTCAAGTGGCAGGCTCAAGGCCATAGCTCAGCATCACGCATATCG 277  
 QY 21 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProAsnGlyAspArgLysArgLys 40  
 Db 338 AGCGATTGCCCTATAGGGACCTACGGCAGGTGGTCAACCCGACAGCATCC 397  
 QY 61 ValIleSerThrProGlnAlaSerLysAlaSerCysLysGlyAlaSerIleSer 80  
 QY :::::::::::::::::::::|||||||:|||||||:|||||||:  
 Db 398 ATGGCTCCACACACAGGGCTCAAGGCCATAGCTCAGCTCAGGACATCACGCATATCG 457  
 QY 81 TyrThrLeuSerArgAsnGlnThrValValAlaGluThrIleSapLysAspThrAsp 100  
 Db 458 TACAGTTCTACGGAGCCAGGGTAGTGGTGAGTACACACGACATTAAGCACAGAC 517

Page 11



RESULT 15  
 US-10-317-250-3  
 ; Sequence 3, Application US/10317250  
 ; Publication No. US20030165945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Cosman, David J.  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; FILE REFERENCE: 2290-B  
 ; CURRENT APPLICATION NUMBER: US/10/317, 250  
 ; CURRENT FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 3  
 ; LENGTH: 1257  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-317-250-3

Alignment Scores:  
 pred. No.: 1 49e-211 Length: 1257  
 Score: 19.7.00 Matches: 342  
 Percent Similarity: 90.5% Conservative: 38  
 Best Local Similarity: 81.4% Mismatches: 38  
 Query Match: 83.7% Indels: 2  
 DB: Gaps: 1

US-10-041-030-4 (1-420) x US-10-317-250-3 (1-1257)

Qy 1 MetPheSerProGlyGluGluGlyCysAlaProAlaLysGluProValIleValGlyAlaThrLeuIleUtpArgTrpGlnAlaAspGly 20  
 Db 1 ATGGTTCTCTCTGTATCAGAAATCAT-----CCATCTAACGCCAGTAAATATGCT 54

Qy 21 GluLeuValValLeuGlyTyroAlaAlaProAlaGlyAspGlyLysGly 40  
 Db 55 GAACTCAATGTCCTAGGATAATAATGGCTCTCCAAACGGTAATAGGAAAGGAA 114

Qy 41 SerArgPheAlaLeuIleUtpAspGlyProLysAlaAsnGlyValIleProSerThrValHis 60  
 Db 115 ArgAGGTTGCTTGTTAAAGCCTAGGCAATGGCTGAGCTGGCACTGCT 174

Qy 61 ValIleSerThrProGlnAlaLeuIleSerCysLysGlyIleSerIleSer 80  
 Db 175 ATGGCTGTTACTCTCAAGCTGCAGCAACAAACGACATACATACATCA 234

Qy 81 TyrThrIleSerArgAsnGlnIleValValIleValGlyIleValIleValGlyAspIleAspThrAsp 100  
 Db 235 TATCTTATCTGGGCCAGACTGTCGTTGAAATACTCATGAGCGCACCGAT 294

Qy 101 MetPheGlnValGlyArgSerThrGluserProIlePheValValIleThrAspThrIle 120  
 Db 205 ArgTTGCAATGCTGGCCGCTGACTGAAACCCATTGTTTGATGACACCGTT 354

Qy 121 SerGlySerGlnAlaThrAspGluIleAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
 Db 355 CTCTGGAAGTCAGAACTAATCTGAACTACAGCTGACTACAGACTATACAGATTGCG 414

Qy 141 CysArgIleValCysAspArgAsnGluIleProIleValIleAlaGlyIlePheAlaAlaGlyPhe 160  
 Db 415 TGCGAATCTATGCTGAAGGAACTCTCCCTTACAGCGGTTTGTCTCAGGTT 474

Qy 161 AspSerSerAsnIlePheLeuGlyGluIleAlaAlaIleSerIleProAspGly 180  
 Db 475 GATCTGATCAAACATCTTCTGGGAGAACTGCTGCAAACTGAGACATCGAGTGA 554

Qy 181 HisMetAspGlyLeuThrIleAspGlyValIleValMetIleProArgGlyGlyPheThr 200  
 Db 535 CAGATGGTGGTGGTGGACCACTATGCTGTCGATGCTCAGGAAATGGGTCACA 594

Qy 201 GluGluSerGlnIleProGlyValIleTrpArgGluIleSerValCysGlyAspValIleThrIle 220  
 Db 595 GAGACTCCTACAGCTGCAATATGGAGGAAATTCGCTGTTGGGAAATGTTACCTA 654

Qy 221 ArgGluIleArgSerAlaIleGlnIleArgGlyIleLeuValGluSerCluIleAspValLeu 240  
 Db 655 CGTGAACACAGATCGGCTTACAGAGGAAATATGGTGAATTCGAAACCATTAGCTA 714

Qy 241 GluAspGlySerIleLeuAspIleCysBGGIleAlaThrIleUtpArgTrpGlnAlaAspGly 260  
 Db 715 CGAGATGCTCTCTTAATGACTCTGCTGCACTTGTGTCAGGCTGAGAGG 774

Qy 261 LeuIpheIleIleProTrpGlyGluIleIleIleGluIleIleIleArgGluIleIleAsnAla 280  
 Db 775 CTTCCTCACCTCTACCGTGAAGCTTACGCTGAGCTTACGCTGAGAGG 834

Qy 281 ArgProGlnCysProValGlyIleLeuIleAlaPheProSerIleAspArgIleGlu 300  
 Db 835 CGACTCTAGTSCCCTGAGGTTCAACACTAGCATTTCTCTAGTGAAGGAGA 894

Qy 301 ValValGluGluIleGluIleProTrpIleAlaPheIleSerCysGlyIleIleGly 320  
 Db 895 GTGCTAGTGAAGAAACACCACTGGATGATTCATGCTGCGCCATCACTGCTCT 954

Qy 321 AsnTrpGlyIleArgSerAspThrGluIleAlaAsnGluIleArgGluIleAsnAla 340  
 Db 955 AACCTGGGAAACAGAAAGGAAACGCTGATGCTGAGTCGATGCTATGCT 1014

Qy 341 ValGlyProTrpValProLeuIlePheLeuGlyCysGluIleAlaGlyPheIleValAspAlaGly 360  
 Db 1015 GTGGCTCTAGTCTCTGAGGCTGAGCTGAGCTGAGCTGAGCTGAGGAGA 1074

Qy 361 ProProThrIleAlaPheIleProCysGlyIleIleValIleGlySerAlaIleIle 380  
 Db 1075 CCTCCAAACCATCGCTTACGGCGTGGGAGTCGTCGAGAAACACTGCTAT 1134

Qy 381 TrpSerCysIleProLeuProIleGlyIleIleValIleAlaIleAlaCysProProCys 400  
 Db 1135 TCTCCCGATCCACTCTCATGGTACTACTTCTACGCTGCTGCTCTTGT 1194

Qy 401 AlaThrGlnIleValGlyGluIleAsnCysIleLeuIlePheGlyGlyProLeuAsp 420  
 Db 1195 GCACTATGTCGCTGAGGAACTACATGACTTATTTCTGAGGACCTCTAGAC 1254

Search completed: March 2, 2006, 07:20:48  
 Job time : 1092 secs

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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: March 2, 2006, 05:56:29 ; Search time 253 Seconds  
 (without alignments)  
 2950.893 Million cell updates/sec

Title: US-10-041-030-4

Perfect score: 2290

Sequence: 1 MFSPGQEEHCAPNPKPVKG.....ATPOLYGEONCIKLIQFOQPID 420

Scoring table: BLOSUM62

Xgapop 10.0 , xgapext 0.5

Ygapop 10.0 , ygapext 0.5

Fgapop 6.0 , fgapext 7.0

Delop 6.0 , delext 7.0

Searched:

1303057 seqs, 888788928 residues

Total number of hits satisfying chosen parameters: 2505114

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\*

Maximum Match 100\*

Listing first 45 summaries

Command line parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

-POSTPROCESSING: Maximum Match 100\*

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-HOSTNAME=US-10-041-030-4 @GEN1-1-193 @runat 0132006\_134408 21912

-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPBEXT=0.5 -FGAPOP=6

-FGAPBEXT=7 -YGAPOP=10 -YGAPBEXT=0.5 -DELOP=6 -DBLEXP=7

Database :

Issued\_Patents\_NA: \*

1: /cgn2\_6/ptodata/l/ina/1\_COMB.seq: \*

2: /cgn2\_6/ptodata/l/ina/5\_COMB.seq: \*

3: /cgn2\_6/ptodata/l/ina/6A\_COMB.seq: \*

4: /cgn2\_6/ptodata/l/ina/6B\_COMB.seq: \*

5: /cgn2\_6/ptodata/l/ina/H\_COMB.seq: \*

6: /cgn2\_6/ptodata/l/ina/PCTUS\_COMB.seq: \*

7: /cgn2\_6/ptodata/l/ina/PP\_COMB.seq: \*

8: /cgn2\_6/ptodata/l/ina/RR\_COMB.seq: \*

9: /cgn2\_6/ptodata/l/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2283	99.7	1263	US-09-843-905A-7
2	2175.5	95.0	1260	US-09-843-905A-5
3	1917	83.7	1257	US-09-843-905A-3
4	1912	83.5	1257	US-09-843-905A-1
5	1642	71.7	1338	US-09-843-905A-11
6	1482.5	64.7	2508	US-10-104-041-1958
7	120.5	5.3	2750	US-08-136-277-1
8	120.5	5.3	2750	US-08-479-403-1
9	120.5	5.3	2750	US-08-835-734-1

\*

Alignment Scores: Pred. No.: 1.38e-238 Score: 2283.00

Percent Similarity: 99.8%

Best Local Similarity: 99.8%

Query Match: 3 DB:

Length: 1263

Matches: 419

Conservative: 0

Mismatches: 1

Indels: 0

Gaps: 0

Sequence 1, Appli

Sequence 2, Appli

Sequence 3, Appli

Sequence 4, Appli

Sequence 5, Appli

Sequence 6, Appli

Sequence 7, Appli

Sequence 8, Appli

Sequence 9, Appli

Sequence 10, Appli

Sequence 11, Appli

Sequence 12, Appli

Sequence 13, Appli

Sequence 14, Appli

Sequence 15, Appli

Sequence 16, Appli

Sequence 17, Appli

Sequence 18, Appli

Sequence 19, Appli

Sequence 20, Appli

Sequence 21, Appli

Sequence 22, Appli

Sequence 23, Appli

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Sequence 25, Appli

Sequence 26, Appli

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Sequence 30, Appli

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Sequence 32, Appli

Sequence 33, Appli

Sequence 34, Appli

Sequence 35, Appli

Sequence 36, Appli

Sequence 37, Appli

Sequence 38, Appli

Sequence 39, Appli

Sequence 40, Appli

Sequence 41, Appli

Sequence 42, Appli

Sequence 43, Appli

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Sequence 50, Appli

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Sequence 55, Appli

Sequence 56, Appli

Sequence 57, Appli

Sequence 58, Appli

Sequence 59, Appli

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Sequence 192, Appli

Sequence 193, Appli

Sequence 194, Appli

Sequence 195, Appli

Sequence 196, Appl

Db 1 ArgTTTCCCCTGCCAGGAGAACACTGCCCCATAAGGGCAGTGAAATCGG 60  
 Qy 21 GlutenuValValLeuIleUglyTyrAlaLysProAlaLysAspArgLysGly 40  
 Db 61 GactGGTGTGTTCTGGGATACAGTGGCTTACCAATGGAGATAGGGAGAA 120  
 Qy 41 SerArgPheAlaLeuTyrLysArgProLysAlaSerGlyAlaLysProSerThrValHis 60  
 Db 121 ASTPAGATTGCCCTCTAGAGGCAATGGTCACACCGTCATGCC 180  
 Qy 61 ValLeuSerThrProGlnAlaSerLysAlaLeuSerCysLysGlyGlnHisSerLe 80  
 Db 181 GigaTATCCACGCCAGGCATCCAACTACAGTCAGCTCAGGTCACAGTATTC 240  
 Qy 81 TyThrIleSerArgArgSerGlnThrValValIleGluLysTyrThrHisAspLysAsp 100  
 Db 241 TACACTTGTCAGGAATCAGACTGAGCTGGTGGAGTACACATGATAAGATACGGAT 300  
 Qy 101 MetPheGlnValGlyArgSerThrProLeuProLeuPheValThrAspPheValThr 120  
 Db 301 ATGTTCAAGGTCAGGATCAAGAAGCCCATCGACTCTGTGTCACACGATT 360  
 Qy 121 SerGlySerGlnAlaThrAspGluAlaGlnLeuThrGlnSerThrLeSerArgPheAla 140  
 Db 361 TCTGGCAGGCAAGCACGGAGGCCAGATCAGCAGGACATTCGGTCC 420  
 Qy 141 CyBargIleValCysBspArgBspArgLysGluProTyrThrAlaArgPheAlaAlaLys 160  
 Db 421 TGCAAGGATGTTGTCAGCAGGAACTACAGCAGGATATGCCCGGGATT 480  
 Qy 161 AspSerSerLysAlaLeuPheLeuIleGluLysGluAlaLysAspSerProAspGly 180  
 Db 481 GACTCTTCAAAACATATTCTGGTAAAGCAGCAAGAAACCCGACGG 540  
 Qy 181 HisMetAspGlyIleThrThrAspGlyValLeuValMetHisProArgGlyGlyPheThr 200  
 Db 541 CACTGAGTCGGCCTACAGTAACTGGCCGCTCTGATCATCACAGGGACTTCAC 600  
 Qy 201 GluGluSerGlnProGlyValLeuPheGluIleSerValCysLysAspValTyrThrIle 220  
 Db 601 GAGGGAGTCCAGGCCCCGGGCTGGGGAGATCTCTGCTGAGATGTTACCTG 660  
 Qy 221 ArgGlutLysArgSerAlaLysGlnGlyLysLeuValGluSerGluThrValAlaLeu 240  
 Db 661 CGAGAAACGAGTCGGCCAGCAAGAAGAACTGGTGTGAAAGTGCACAACTGCTG 720  
 Qy 241 GluAspGlySerIleLeuAspLeuCysGlyAlaThrLeuLeuTrpArgThraAlaAspGly 260  
 Db 721 CAGGACGGCTCCCATGGCTCTGGGCACTCTCTGGAGAACAGAGATGG 780  
 Qy 261 LeuLeuHisIleThrProArgLysIleLysIleGluAlaLeuArgGlnGluLeuAlaAla 280  
 Db 781 CTTTTCATACTCCAACTCAGAACATAGAACCCCTCGGGGGAGATTACGCC 840  
 Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlaPheProSerIleLeuAspGlyGlu 300  
 Db 841 CGCTCTACTGTCCTGGCTCAACACCTGCTGCCCTCAGCATCACAGAAG 900  
 Qy 301 ValValGluGluLysBglnProTrpAlaTyroLeuSerCysGlyHiIvalHisGlyTyHis 320  
 Db 901 GTGGTGGAGGAAGGAGCCCTGGGATCTCAGTGTGGCCAGTGACGGTACAC 960  
 Qy 321 AsnTrpGlyHisArgSerAspThrGluIaAsnGluArgGluCysProMetCysArgThr 340  
 Db 961 ACTCTGGGCCATCCGGTAGAACCGAGGCCAACAGGAGGAGTCACCCATGTCAGGACT 1020  
 Qy 341 ValGlyProTrpValProLeuProLeuGlyCysGluAlaLysPheTrpValAlaPheAla 360  
 Db 1021 GTGGGCCCCATGTCCTCTGTCCTGAGGAGTTATGTCAGGAGCA 1080  
 Qy 361 ProProTrpHisAlaPheThrProCysGlyHisValCysSerGluLysSerAlaLysTyr 380  
 Db 1081 CGCCAACTCTGCTTCACTCCCTGGAACGCTGTCGGAGAACGCTGCAAAATC 1140

Qy 381 TrpSerGlnLeuProLeuProLysGlyThrHisAlaPheHisAlaAlaCysProHeCys 400  
 Db 1141 TGGTCAGATCCGGTTCATGAACTCATGCAATTCTCGTCCTTCCTG 1200  
 Qy 401 AlaThrGlnLeuValGlyGluGlnAsnCysTyleLeuLeuPheGlnGlyProLeAsp 420  
 Db 1201 GCTACAGAGCTGTGGGAGCAACTGCATCAATTTCAGGTCAAATGAC 1260  
 RESULT 2  
 US-09-843-905A-5  
 ; Sequence 5, Application US/9843905A  
 ; Patent No. 6703487  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; FILE REFERENCE: 2990-A  
 ; CURRENT APPLICATION NUMBER: US/09/843, 905A  
 ; CURRENT FILING DATE: 2001-04-27  
 ; PRIOR APPLICATION NUMBER: US 60/200, 198  
 ; PRIOR FILING DATE: 2000-04-28  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 5  
 ; LENGTH: 1260  
 ; TYPE: DNA  
 ; ORGANISM: Mus musculus  
 ; US-09-843-905A-5  
 Alignment Scores:  
 Pred. No.: 7.05e-227  
 Score: 2175.50  
 Percent Similarity: 97.4%  
 Best Local Similarity: 95.0%  
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 DB: 3  
 Qy 201 GluGluSerGlnProGlyValLeuPheGluIleSerValCysLysAspValTyrThrIle 220  
 Db 601 GAGGGAGTCCAGGCCCCGGGCTGGGGAGATCTCTGCTGAGATGTTACCTG 660  
 Qy 221 ArgGlutLysArgSerAlaLysGlnGlyLysLeuValGluSerGluThrValAlaLeu 240  
 Db 661 CGAGAAACGAGTCGGCCAGCAAGAAGAACTGGTGTGAAAGTGCACAACTGCTG 720  
 Qy 241 GluAspGlySerIleLeuAspLeuCysGlyAlaThrLeuLeuTrpArgThraAlaAspGly 260  
 Db 721 CAGGACGGCTCCCATGGCTCTGGGCACTCTCTGGAGAACAGAGATGG 780  
 Qy 261 LeuLeuHisIleThrProArgLysIleLysIleGluAlaLeuArgGlnGluLeuAlaAla 280  
 Db 781 CTTTTCATACTCCAACTCAGAACATAGAACCCCTCGGGGGAGATTACGCC 840  
 Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlaPheProSerIleLeuAspGlyGlu 300  
 Db 841 CGCTCTACTGTCCTGGCTCAACACCTGCTGCCCTCAGCATCACAGAAG 900  
 Qy 301 ValValGluGluLysBglnProTrpAlaTyroLeuSerCysGlyHiIvalHisGlyTyHis 320  
 Db 901 GTGGTGGAGGAAGGAGCCCTGGGATCTCAGTGTGGCCAGTGACGGTACAC 960  
 Qy 321 AsnTrpGlyHisArgSerAspThrGluIaAsnGluArgGluCysProMetCysArgThr 340  
 Db 961 ACTCTGGGCCATCCGGTAGAACCGAGGCCAACAGGAGGAGTCACCCATGTCAGGACT 1020  
 Qy 341 ValGlyProTrpValProLeuProLeuGlyCysGluAlaLysPheTrpValAlaPheAla 360  
 Db 1021 GTGGGCCCCATGTCCTCTGTCCTGAGGAGTTATGTCAGGAGCA 1080  
 Qy 361 ProProTrpHisAlaPheThrProCysGlyHisValCysSerGluLysSerAlaLysTyr 380  
 Db 1081 CGCCAACTCTGCTTCACTCCCTGGAACGCTGTCGGAGAACGCTGCAAAATC 1140

Pred. No.: 1-02e-198 Length: 1257  
Score: 1917.00 Matches: 342  
Percent Similarity: 90.5% Conservative: 38  
Best Local Similarity: 81.4% Mismatches: 38  
Query Match: 83.7% Indels: 2 DB:  
Gaps: 1

US-10-041-030-4 (1-420) x US-09-843-905A-3 (1-1257)

Qy 1 MetPheSerProGlyIleGluLysCysBalaProbabljygluProvallystYgLy 20  
Db 1 ArgGluThrArgSerAlaGlnGluLysIleGluLeuValMetIleProArgGlyLys 20  
Qy 221 ArgGluThrArgSerAlaGlnGluLysIleGluLeuValMetIleProArgGlyLys 20  
Db 658 CGAGGACAGGGTGGCCAGCAG 717  
Qy 241 GluAspGlySerLeuIleAspLeuCysGlyValThrLeuLeuLeuLeuLeuLeu 260  
Db 718 CAAGAGGCTCCCTCATGACTGTGTTGGCCACTCTGCCTGGAGAACGGATGAC 597  
Qy 261 LeuPheHisThrProThrGlnLysIleGluIleLeuLeuArgGlnGluIleLeu 220  
Db 778 CTTTCAGCTCTACTCGAGCACATGAGCCCTCGGCCAGGATCAATCAGCC 837  
Qy 281 ArgProGlnCysProValGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 280  
Db 838 CGACCCGAGTGGCCGTCGAC 897  
Qy 301 ValValGluGluIleGlnIleProValAlaPheProSerIleLeuArgIleGlu 320  
Db 898 GCGTGAGAGAGAGAGCAGCCTGAGCTGAGCTGGGGAGCTGAGCTGAGC 957  
Qy 321 AsnTrpGlyIleAspSerAspThrGluIleAspGluIleAspGluCysProMetCysArgThr 340  
Db 958 AGTTGGGCCATGGAGCAGCCAAAGCCACCTGCTGAGGACTTCCTGTCGAGCT 1017  
Qy 341 ValGlyProTyroValProLeuTrpLeuGlyCysGlyIleAlaGlyProLeu 360  
Db 1018 GTCGGCCCTACGTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1077  
Qy 361 ProProTrpIleAlaPheThrProCysGlyIleValCysSerGlyIleSerAla 380  
Db 1078 CCCCOAACTCACGCTTCACCCCCTGCGGACCTCTGTCAGAAAGTCGCAAGTAC 1137  
Qy 381 TrpSerGlnIleProLeuProHisAlaAlaAlaCysProHeCys 400  
Db 1138 TGGTCCGAGATCCCTGCCCCACCGAACCCGGTTTCATGCCCTTCCTGCTG 1197  
Qy 401 AlaThrginIleLeuValGlyIleGlnIleCysValLeuLeuLeuLeuLeu 420  
Db 1198 GCGACGCACTGGTTGGACAGACTGCATCAATTGATTTCAGTCAGTGGAC 1257  
RESULT 3  
US-09-843-905A-3  
; Sequence 3, Application US/09843905A  
; Patent No. 6703487  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; CURRENT APPLICATION NUMBER: US/09/843,905A  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,198  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SRQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1257  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-843-905A-3





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Db 262 ----- ATC 264  
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TCCACGGCCGCTCTCTCCAGGACTGAGTAACCGTGATCACGACAGCATCTCGTATCA 324  
Db 265 LeuSerArgArgBlnInthrValValValGluTyThrIleAspIleSerIleSerTyThr 82  
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83 CTCAGTGGCCGAGCCACTGCTATGAGATGAGATCACATGATGACTTCGCGTACAGACACATGTC 384  
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CTGTGCCCGAGCCACTGCTATGAGATGAGATCACATGATGACTTCGCGTACAGACACATGTC 384  
QY 103 GluValGlyArgSerSerThrGluSerProLeuAspPheValIleAspThrAspMetPhe 102  
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385 CGATTGGCCGCTCACAGAGACATGATGACTTCGCGTACAGACACATGTC 444  
Db 123 SerGlnAlaBlnThrAspGluLysGlnIleIleThrGlnSerArgSerThrIleSer 142  
ATCCCTCTGGAGCCGCCAACCTATACTGCCGCATTAACCGCTGCTGTTGAGGCC 561  
Db 445 GGA---GGGGCTGCCGAGGCCCTCTGCCAGAGACATCTCCGCTATGCTGCGC 501  
QY 143 IleValCysAspArgAspGluProTyrrThrAlaArgIlePheAlaAlaGlyAspSer 162  
|||||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
Db 502 ATCCCTCTGGAGCCGCCAACCTATACTGCCGCATTAACCGCTGCTGTTGAGGCC 561  
QY 163 SerIleBlnIlePheLeuGlyGluLysAlaAlaLysTrpIleAspGlyIleMet 182  
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Db 562 TCTAGCACATCTTCTTGTGAAAGCGACGCCAAATGCGAACCCAGATGCCATG 621  
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QY 183 AspGlyLeuThrThrAspGlyValMetIleHisProArgGlyGlyPheThrGlu 202  
622 GATGACTGACTGACCACCAATGAGTCCTGGTGTGATGCCACCCGCAACCGGCTCTCCGAGAC 681  
QY 223 ThaArgSerAlaGlnGlnArgIleLysValLeuAlaLysSerGluIleAspThrAsp 242  
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Db 742 AGCCGCTGAGCCAGACGGGCAAGCTGTTGAAAGCGAACGCCAACGTCGAGAC 801  
QY 243 GlySerLeuIleAspLeuCysGlyIleAlaThrLeuIleAspGlyValLeuGly 262  
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Db 263 HisIleProThrGlnLysIleIleGluAlaIleLeuIleAspGlyLeuIle 282  
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1222 GCCCAAGACACCACTGCGGCCAGGACACCCGCTTCGCGCTGCCCTGCGGCCCTGCG 1281  
402 ThrGlnLeuValGlyGluLysAsnCysIleIleLeuIlePheGlnGlyProIleAsp 420

Db 1282 GCCTGGCTTACCGGGAGCATGGCTCGCCCTCATTTCCAGGCCCGCTGGAT 1338  
RESULT 7  
US-08-136-277-1  
; Sequence 1, Application US/08136277  
; Patent No. 5634045  
; GENERAL INFORMATION:  
; APPLICANT: MANDEL, Jean-Louis  
; APPLICANT: AUBOURG, Patrick  
; APPLICANT: MOSSER, Jean  
; APPLICANT: SARDIE, Claude  
; TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND  
; TITLE OF INVENTION: CORRESPONDING PROTEIN  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Young & Thompson  
; STREET: 745 South 23rd Street  
; CITY: Arlington  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/136,277  
; FILING DATE: 15-OCT-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PATCH, Andrew J.  
; REGISTRATION NUMBER: 32,925  
; REFERENCE DOCKET NUMBER: B2272  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-521-2297  
; TELEFAX: 703-685-0573  
; TELEX: 248425 EMBON  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2750 base pairs  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 387..2624  
; US-08-136-277-1  
Alignment Scores:  
Pred. No.: 0.0186 Length: 2750  
Score: 120.50 Matches: 104  
Percent Similarity: 33.9% Conservative: 63  
Best Local Similarity: 21.1% Mismatches: 155  
Query Match: 5.3% Indels: 171  
DB: 2 GlnValValLeuGlyLysIleAspGlyValLeuIleAspGlyLeuIleAsp 2750  
US-10-041-030-4 (1-420) x US-08-136-277-1 (1-2750)  
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Db 1167 TTCTCGCC-----  
QY 22 LeuValValLeuGlyLysIleAspGlyValLeuProAsnGlyIleAspArgGlyIleSer 41  
Db 1188 CTGGTG-----  
QY 42 ArgPheAla---LeuTyryLysArgProLybalAAsnGlyValLeuProSerThrValHis 60  
Db 1218 GACCTGCCTACATGCACTCGGGGTTGCTGGCGCAAC----- 1253

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Db 2261 CGCTTCCCTGATGATGCCACAGC-----|||CCGGAGG
`Qy 362 -----
Db 2300 CGTGGAAAGCAAGATCTTCAGGGCCAAAGAACGGGGCATGGCTGCTCTCCTG-----|||C
Qy 364 1sAlaPheThrProCysGly-----HisValCys-----|||C
Db 2360 CCACCGGCCTCCCTGGAAATCACACACATGTGCTACAGTTGATGGGAC-----|||C
Qy 375 IulysSerAlaLyTyrTpSerGlnIlePro 385
Db 2420 CTGGAAAGTCAGAGACTCGACTCAGCTGCC 2451

RESULT 8
US-08-479-403-1
; Sequence 1, Application US/08479403
; Patent No. 5869039
; GENERAL INFORMATION:
; APPLICANT: MANDEL, Jean-Louis
; APPLICANT: AUBOURG, Patrick
; APPLICANT: MOSER, Jean
; APPLICANT: SARDE, Claude
TITLE OF INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Young & Thompson
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479, 403
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32, 925
REFERENCE/DOCKET NUMBER: B2272DIV

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEX: 248425 EMBON
TELEFAX: 703-685-0573

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2750 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 387..2624
; US-08-479-403-1
; Alignment Scores:
Pred. No.: 0.0186 Length: 2750
Score: 120.50 Matches: 104
Percent Similarity: 33.9% Conservative: 63
Best Local Similarity: 21.1% Mismatches: 155
Query Match: 5.3% Indels: 171
DB: Gaps: 26
US-10-041-030-4 (1-420) x US-08-479-403-1 (1-2750)

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QY 2 PheserProGlyGingluLuisCysAlaProAlnlysGluProVallysTyrglAlu 21  
 Db 1167 |||||-----AAGTGGGAG 1187  
 QY 22 LeuvalValleuGlyTyraBnGlyAlaLeuProAlnGlyAspArglyArgArglySer 41  
 Db 1188 Ctreotg-----GCAGAGGGCCGGGAAGGG 1217  
 QY 42 Argpheala--LeutyrylsarqProlysAlasnglyVallysProserthrvalhis 60  
 Db 1218 GAGGTGCGCTACAGCACTCGCGTGGTGGCCAC----- 1253  
 QY 61 ValileSerthrProGlnAlaSerlysAlaIleserCysLysGlyGlnHisSerileser 80  
 Db 1254 -----TCGAGGAGTCGCCCTATGGGSCATGAGTG 1292  
 QY 81 TyrThrLeu-----SerArgLysGlnThrValValval 91  
 Db 1293 CTGGCCCTCTACAGGCCCTACAGGACCTGGCTCCAGATCACCTCTCTCTG 1352  
 QY 92 Glu-----TyrThrHisAlpLysAspThrAspMetPhenylalanylGlyArgSerThr 108  
 Db 1353 GAAGCCCTGTGTAATGCTGAGCATGTCATGAGATGATGTCAGGAGGCCCTG 1412  
 QY 109 GluserProIeasPheValValthrephthileSerGlyBargIleValCysAspArgin 148  
 Db 1413 GGCTGCTCATGGGCTCCATCACAATGCCATGCTCACTGGCTACTCAGAGTCAGTG 1472  
 QY 1473 GAGGCCGAGAAGGAGGCCCTGGAAAGAAGAGGAGGAGGAGGTTGGAGGGAGGCA 1532  
 QY 149 GluProTyrThr-----AlaArgIleHeAlaLaglyPheAspSerSerlysAsnile 166  
 Db 1533 GAAGCCTTCACTATTGCCGCAACCTCTGAGACGGGCTGAGATGCCATTAGGGATC 1592  
 QY 167 -----PheneuGlyAluLysAlaLysAlpLysBnProAspGlyAlisMetAsp 183  
 Db 1593 ATGRCGTCGCTA-GGAGTGGACGGACTGCGCTACACGCCCGGTGACAGAT 1651  
 QY 184 -----GlyLeu----- 185  
 Db 1652 GTTCAGGATTGAGATGTCAGGCCCTACTCAGAGGCCAGGGCTAGAGGA 1711  
 QY 186 ThrThrAsnGlyValleu-----ValMethIspProArgGlyGlyPheThrAlu 201  
 Db 1712 CGCTCAGGGGGGCTGCGACCATAGGCCGGTCTGGCTGCGTGTGGAGGCCCTGAA 1771  
 QY 202 GluserGlnProGlyValItpArgGluIleSerValCysGlyAspValtyrThrLeuarg 221  
 Db 1772 GATCGAGGCCAGT-----GAGGATGAGACAGGEGATCATCGGA 1816  
 QY 222 Glu-ThrArgSerAlaGlnGlnArglyTysLeuValGluSerGluThrAsnVal--Le 240  
 Db 1817 GAACATCCCCATCTCACCCCTCAGGAGGTTGGCCAGCTCAACATCAGGT 1876  
 QY 240 uGlnAspGly-----SerLeuI 246  
 Db 1877 GAGGAGGCCATCTCACAGCCCCAATGCTGCCAACAGCTACAGGCCCT 1936  
 QY 246 eAspLeuCysGlyAlaThrIleLeutParglrrAlaAspGlyLeuPheHisthrProH 266  
 Db 1937 CGCGATCCCTGGCTGG-----CTGCGCCACGCTGCTGCTGCTACAGGCCCT 1990  
 QY 266 rGlnLysHsIleLgluLalaLeuArgGlnGluIleAsnAlaAlaArgProGlnCysPro 286  
 Db 1991 ACCCGCCATGTCATCTCACATCCGGCAG-----AGGCCCTACITGTCGT 2035  
 QY 286 lsgly-----LeuSerThrLeuAlaPheProSerIleAsnArgLysGluValValGluI 304  
 Db 2036 GGCGCCCTGGCTGACCAAGGTTGATCTACCGG-----GACTCACTGGAGGA 2080  
 QY 304 uLySGLnProTrpAlaTyr-----LeuSerCysGlyLysIva 316

RESULT 9  
 US-08-835-734-1  
 ; Sequence 1: Application US/08835734  
 ; Patent No. 6013769  
 GENERAL INFORMATION:  
 APPLICANT: MANDEL, Jean-Louis  
 APPLICANT: AUBORG, Patrick  
 APPLICANT: MOSSER, Jean  
 APPLICANT: SARDE, Claude  
 TITLE OR INVENTION: X-LINKED ADRENOLEUKODYSTROPHY GENE AND  
 NUMBER OF INVENTION: CORRESPONDING PROTEIN  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Young & Thompson  
 STREET: 745 South 23rd Street  
 CITY: Arlington  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22202  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/835,734  
 FILING DATE:  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/479,403  
 FILING DATE: 07-JUN-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PATCH, Andrew J.  
 REGISTRATION NUMBER: 32,925  
 REFERENCE DOCKET NUMBER: B2272DTV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-521-2297  
 TELEFAX: 703-685-0573  
 TELEX: 248425 EMBO  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2750 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: Single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA





APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 10716-136  
CURRENT APPLICATION NUMBER: US/09/252, 991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074, 788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094, 190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SSEQ ID NO 14397

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 ; SEQ ID NO: 14280  
 ; LENGTH: 3801  
 ; TYPE: DNA  
 ; ORGANISM: *Pseudomonas aeruginosa*  
 ; US-09-252-991A-14280  
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 Db 251 LysThrLeuIleTrpArgThr--AlaAspGlyLeuPheHisThrPro-----G 243  
 Qy 902 TGAATCATCAGGAGAGATGCCAGGAGTCGCCAGGATGCCCTCGGG 849  
 Db 788 CCAAGGCGCTGGAGCTGGCGGCGGAGGATGCCGCTGCCTCGGG 849  
 Qy 243 LysSerLeuIleAspLeuCysGly-----A 251  
 266 -----ThrGlnLysBistIleGluAlaLeuArgGlnGluLe----- 277  
 Db 728 CCTCCAAGGCCAGGAGACGCCGCGGCAATTCCGAGCTGCCAGGCGGCCACCTGC 669  
 Qy 278 -----AsnAlaLysLysLeuAspGlyLeuProGlnCysPro 286  
 Db 668 CGGTATGGCTACACAACCGCGATCTACCGAACGACTCCG 609  
 Qy 286 alGlyLeu-----AsnThrLeuAlaPhe-----ProSerIleAsnArglyG 300  
 Db 608 TTCTCTGCGACTGCGAGAACTGTTGCTCTGCTCTGAAAGCACGCT 549  
 Qy 300 luValValGluGluLysGlnPro-TrpAlaTyroLeuSerCysGlyLysIvalHisGlyTyr 319  
 Db 548 GCTTATCGACGTAAGCACCAGGTTGGCGAGCCCTCATCTCTTCG---CCCGCTCG 492  
 Qy 320 HisAsnTrpIleHisArgSer-----AspThrGluAlaAsnGluLysGluCysPro 336  
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 Qy 337 MetCys----- 338  
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 Qy 339 -----ArgThrValGlyProTyroValProLeu 347  
 Db 371 AGGGATGGCGATCTAACGAGTGGCTGATGCCGATCTCCGACGCCGCTCCGACC 312  
 Qy 348 TrpIleGlyCysGluAlaIleGlyPheThrValAspAlaGlyPro----- 361  
 Db 311 TGG-----TGAGTGCATCAAGCTCTGGGAGCACTCGCGGTTGGGGAGGCTCA 258  
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 US-09-252-991A-14280  
 ; Sequence 14280, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 10196-136  
 ; CURRENT APPLICATION NUMBER: US-09/252, 991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074, 788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094, 190  
 ; PRIOR FILING DATE: 1998-07-27





Db 32625 - GTC ACT CCAGG CAGG AAT TGG GAA ACAC AGA AGCT CA 32586  
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 Db 32585 AGCCGAAGGCCAGCCACCAAGCAGCAGCAGCGGGTGGGACCCGACCATAC 32526  
 Qy 291 - IeAlaLpheProSerIleAsnArgLysGluValValGluGluLysGlnP 307  
 Db 32525 CGAGCCCTGGCAAGCAGCCCGAGCAGCTGCAGGAGACTGAGCTTCAGAGGGAGAC 32466  
 Qy 307 rOrtPAlaTyreLeuSerCysArgLysIleValIleGlyTyRHisAsnTrpGlyHisArgSerA 327  
 Db 32465 AGCCCCAGCTCTCACGATGTTGGGCTCTGTGAACTGGGT----- 32416  
 Qy 327 SphIrrGluAlaAengluArgGlycProMetCysArgThrValGlyProTrpValProL 347  
 Db 32415 - GACCCCGCAGATGGCAGAACCCAGGC-----TTTGTCCTA- 32380  
 Qy 347 eutTrp-----LeuGlyCysGluAlaAglYPhetYrValAspAlaGlyP 361  
 Db 32379 - TAGGGCTCTGGTCCAGCTTGACTGTAATACTGGTC--TAGGACCCATTC 32325  
 Qy 361 rOrPProThrHisAlaPheThrProCysGlyHisIleValCysSerGluLysSerAlaLys 379  
 Db 32324 CAGTCAGACAGGCCAGAAACCATGGGTCAACCAGTGGGAGGCCAGCAAG 32269

Search completed: March 2, 2006, 09:43:27  
 Job time : 3232 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: March 2, 2006, 05:14:56 ; Search time 5360 Seconds  
 (without alignment)  
 3666.152 Million cell updates/sec

Title: US-10-041-030-4  
 Perfect score: 2290  
 Sequence: 1 MFSPGQEEHCAPNPKPVKYG.....ATQOLVGEONCNIKLIQGPID 420

## Scoring table:

Xgapop	xgapext	Ygapop	Ygapext	Fgapop	Fgapext	Delop	Delext
10.0	0.5	10.0	0.5	6.0	7.0	6.0	7.0

searched: 41078325 seqB, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq. length: 0  
 Maximum DB seq. length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:  
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 -O=/abs/ABSSWEB/spool/US10041030/runat 01032006\_134406\_21863/app\_query.fasta\_1  
 -DB=BEST -QWRT=flatap -SURPIX=p2n.RT -MINMATCH=0.1 -LOCFCI=0 -LOCFCXT=0  
 -UNITS=bits -START1=1 -END1=1 -MATRIXK:blosum62 -TRANS=human40.cal -LIST=45  
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 -USER=US10041030 @CGN\_1\_1\_5315 @runat 01032006\_134406\_21863 -NCPU=6 -ICPU=3  
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 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=0 -KGAPRT=0.5 -FGAPOP=6 -FGAREXT=7  
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Db	1022	ACTCCCTGAGCACAGTGTGTCAGCAATATCGTCAGTCAGTCGGTG	1081	Ds	122	GCCTCCAGGCCATCAGCTCCAGAGACATCACAGCATATCCTACCGTGACGGC	181
Oy	387	ProHsGLYRhrHsAlaPheHsAlaAlaCysProHeCysAlaThrGlnLeuValGly	406	Oy	87	GlnThrValValGluValGluTyrrHsAspLysAspThrAspMetPheGlnValGly	106
Db	1082	CCTCATGGAACTCATGCAATTTCAGCTTCTGCTTCAGCTACAGCTGTTGGGG	1141	Ds	182	CAGACGGTAGTGTGAGGATCACACGATAAAGACACGGACATGTTAGGTGGCG	241
Oy	407	GluGlnAspCysIleLeuLeuPheGlnGlyProLeAsp	420	Oy	107	SerThrGluSerProLeAspPheValIleAspThrIleSerGlySerGlnThr	126
Db	1142	GAGCAAACCTGATCAAAATTTCAGGTCATGAC	1183	Ds	242	TCAACAGAAAGCCCATTTGACTTCGTTGACAGACAGCTGGT	301
<b>RESULT 3</b>							
LOCUS	AY409118	AY409118	1183 bp	DNA	1183 bp	DNA	1183
DEFINITION	Mus musculus PEL12 gene.	VIRTUAL TRANSCRIPT,	partial sequence,				
ACCESSION	AY409118	genomic survey sequence.					
VERSION	AY409118.1	GI:39765086					
KEYWORDS	GSS.						
SOURCE	Mus musculus (house mouse)						
ORGANISM	Mus musculus						
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Butcher; Burchong; Gires; Rodentia;						
1	(bases 1 to 1183)						
Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,							
Todd,M.A., Tannenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,							
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Srinakay,J.J.,							
Adams,M.D. and Cargill,M.							
Inferring nonneutral evolution from human-chimp-mouse orthologous							
gene trios							
JOURNAL	Science 302 (5652), 1960-1963 (2003)						
PUBLMED	14671302						
REFERENCE	2 (bases 1 to 1183)						
AUTHORS	Clark,A.G., Golanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,						
Todd,M.A., Tannenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,							
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Srinakay,J.J.,							
Adams,M.D. and Cargill,M.							
TITLE	Direct Submission						
JOURNAL	Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive,						
COMMENT	Rockville, MD 20850, USA						
This sequence was made by sequencing genomic exons and ordering							
them based on alignment.							
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Alignment Scores:							
Pred. No.:	3.84e-196	Length:	1183				
Score:	2052.50	Matches:	375				
Percent Similarity:	97.7%	Conservative:	10				
Best Local Similarity:	95.2%	Mismatches:	8				
Query Match:	89.6%	Indels:	1				
DB:	10	Gaps:	1				
US-10-041-030-4 (1-420) x AY409118 (1-1183)							
Oy	27	TYRArgLYIAlaLeuProArgGlyAspArgVArgArgLysSerArgPheAlaLeuPyr	46	Oy	347	LeuTrpLeuGlyCysGluAlaLysPheTyrrValAspAlaLysPheProThrHisAlaPhe	366
Db	2	TACCATGGCTCTTACCTATGGTGTGAGCGGCGAGAACGAGTTCCTCTAT	61	Ds	959	CTCTGGCTGGCTGTGAGCAGGATTATGCGATGCGGACCCCACCTCACGCTTC	1018
Oy	47	LysArgProLysAlaAlaGlyValLeuSerThrValSerThrProGln	66	Oy	367	ThrProGlyHisValCysSerGluLysSerAlaLysThrPheSerGlnIleProLe	386
Db	62	AGCGGACCTAACGAGCTGTCACAGCCACATCACATGCTTCACACCACAG	121	Ds	1019	ACCCCTGGGGCACGCTGTCAGAAAGTGCCAGACTGCTGCTGCCCCCTACGTCCT	958
Oy	67	AlaSerLysAlaLeuSerCysLysArgGlyGlnHisSerIleSerTyrrThrLeuSerArgAsn	86	Oy	1079	CCCCAGGAACGCGCCGTTCAAGCCCTGCGCTTCGGCCACGAGCTGGTGT	1138
RESULT 4							
LOCUS	AK045515		3530 bp	mRNA	linear	HTC 03-APR-2004	

DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230208C14 product:pellino 2, full insert sequence.		
ACCESSION	AK045515		
VERSION	AK045515.1 GI:26090937		
KEYWORDS	HTC; CAP trapper; Mus musculus (house mouse)		
SOURCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murine; Mus.		
REFERENCE	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636		
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000) 11042159		
PUBLMED			
REFERENCE	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsumi,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,S., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujikake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsubara,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
AUTHORS	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000) 11076861		
PUBLMED			
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001) 5		
AUTHORS	The RIKEN Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 3530)		
JOURNAL	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Harai,A., Hashizume,W., Hayashida,K., Hayashi,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Konda,M., Koya,S., Kuwahara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Ohnato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tademi,M., Tomaru,A., Takeda,Y., Tanaka,T., Tomaru,A., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-12-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-reseqsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.		
FEATURES	URL: <a href="http://fantom.gsc.riken.jp/">http://fantom.gsc.riken.jp/</a> location/Qualifiers		
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PRED. NO.:	1 23e-182	LENGTH:	3530
SCORE:	126.00	MATCHES:	361
PERCENT SIMILARITY:	87.4%	CONSERVATIVE:	6
BEST LOCAL SIMILARITY:	86.0%	MISMATCHES:	9
QUERY MATCH:	84.1%	INDELS:	45
DB:	4	GAPS:	2
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Db	352 GAGCTGGGGTCT-GGG-----	368	
QY	41 SerArgRheAlaIleTyrLysArgProIysAlaAsnGlyValIysProSerThrValHis	60	
Db	368 -----	368	
QY	61 ValLeuSerThrProGlnAlaSerAlaSerSerOxyLysGlyGlnHissSerIleSer	80	
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QY	81 TyrThrIleSerArgAspArgLysThrValValValGlyLysThrIleAspLysBpThrAsp	100	
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QY	GATCTCTCCAAATAATCTTCTTGAGAGAGACAAATGGAAAACCTGTGAGGA 698	181 HisMetAspGlyLeuThrThrAsnGlyValLeuAlaMetBpArgGlyGlyPhthr	200
Db	699 CACCTGGATGGACTCTACCACGGCTCTCTGTGAGCACCGCAGGAGGACTTCAC 758		

- |                     |   |
|---------------------|---|
| AUTHORS             | Carninci, P., Shibata, K., Aizawa, K., Nagacka, S., Sasaki, N., Carninci, P.  |
| TITLE               | Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  |
| JOURNAL             | Genome Res. 10 (10), 1617-1630 (2000)   |
| PUBLISHED           | 11/04/2000  |
| REFERENCE           | 3 Carninci, P., Shibata, K., Aizawa, K., Nagacka, S., Sasaki, N., Carninci, P., Itoh, M., Konno, H., Ohzaki, Y., Muramatsu, M., Inoue, K., Tanaka, T., Matsunaga, S., Kawai, J., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikeuchi, T., Kashiro, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, K., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer |
| Db                  | 819 CGAGGACCGAGGCCCCAGCAGGGAAAGTGAGCAATCTCTG 878  |
| Qy                  | 241 GluGluSerGlnProGlyValTyrArgGluIleSerValCysGlyAspAlaThrLeu 220   |
| Db                  | 759 GAGGATCCGAGCTGAGCTCTGGAGAGATCTCTCTGAGATCTACCTCTG 818  |
| Qy                  | 221 ArgGluThrArgSerAlaGlnGluArgGlyLysIleValGluSerGluThrAsnValLeu 240  |
| Db                  | 939 CTTTTCAGCTCTACTCTGAACCTGCTGGAGCTCAATCCAGGCC 998   |
| Qy                  | 281 ArgProGlnCysProValGlyLeuSerThrLeuAlaPheProSerIleLeanArgYngCiu 300   |
| Db                  | 999 CGACCCCCAGTCCCCGGGGCTTAACACCTGGCTTCCCAGCATCAC 1058  |
| Qy                  | 301 ValValGluGluIlyBglInProtTalaTrileuserCysGlyHisValHiBglYtrHs 320   |
| Db                  | 1059 GTGCGTGGAAAGAGCAGCAGCCCTGGCACTCTGAGAATGCGAGATGCC 938   |
| Qy                  | 321 AsnTrpGlyIlyIleSerAspThrGluAlaAsnGluArgGluCpProMetCysArgTrp 340   |
| Db                  | 1119 AGCTGGGCCATGGAGGCAACGGAAAGCCCTGGCGAGGAGTCATCCAGGCC 1118  |
| Qy                  | 341 ValGlyProTrpValProLeuTrpLeuGlyCysGluIalAglyPheTrpValAlaGly 360  |
| Db                  | 1179 GTGAGCCCCAACGCTCTGCTGGCTGTGGAGGATTATGCGAGCCGGGA 1238   |
| Qy                  | 361 ProProTrpIleAlaPheThrProGlyHisValCysSerGluIleSerAlaIleCysProHeCys 400   |
| Db                  | 1299 TGGTGCAGATCCCCTGCTGCCACCGAACGGCACGGTTTACGGCGCTGTCCCTCTGC 1358  |
| Qy                  | 401 AlaThrGlnLeuValGlyGluGlnAsnCysLeuIlePheGlnIlyProLeuSp 420   |
| Db                  | 1359 GCCAGGCACTGGTTGGTACAGACACTGCATCAAATGATTTCAGTCCAGTGGAC 1418   |
| RESULT 5            |   |
| LOCUS               | AK045673  |
| DEFINITION          | Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230220E21 product:pellino 1, full insert sequence.  |
| ACCESSION           | AK045673  |
| VERSION             | AK045673.1  |
| KEYWORDS            | HTC; CAP trapper.   |
| SOURCE              | Mus musculus (house mouse)  |
| ORGANISM            | Mus musculus  |
| BIOLOGICAL_ASSEMBLY | BioProject: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteroidea; Bucroentocephaloidea; Sciuromorphati; Muridae; Murinae; Mus.   |
| REFERENCE           | 1 Carninci, P. and Hayashizaki, Y.  |
| AUTHORS             | Carninci, P. and Hayashizaki, Y.  |
| TITLE               | High-efficiency full-length cDNA cloning  |
| JOURNAL             | Meth. Enzymol. 303, 19-44 (1999)  |
| PUBLISHED           | 10/34/1996  |
| REFERENCE           | 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Ohzaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  |
| Qy                  | 241 GluGluSerGlnProGlyValTyrArgGluIleSerValCysGlyAspAlaThrLeu 220   |
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| Qy                  | 221 ArgGluThrArgSerAlaGlnGluArgGlyLysIleValGluSerGluThrAsnValLeu 240  |
| Db                  | 939 CTTTTCAGCTCTACTCTGAACCTGCTGGAGCTCAATCCAGGCC 998   |
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| Qy                  | 301 ValValGluGluIlyBglInProtTalaTrileuserCysGlyHisValHiBglYtrHs 320   |
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| Qy                  | 321 AsnTrpGlyIlyIleSerAspThrGluAlaAsnGluArgGluCpProMetCysArgTrp 340   |
| Db                  | 1119 AGCTGGGCCATGGAGGCAACGGAAAGCCCTGGCGAGGAGTCATCCAGGCC 1118  |
| Qy                  | 341 ValGlyProTrpValProLeuTrpLeuGlyCysGluIalAglyPheTrpValAlaGly 360  |
| Db                  | 1179 GTGAGCCCCAACGCTCTGCTGGCTGTGGAGGATTATGCGAGCCGGGA 1238   |
| Qy                  | 361 ProProTrpIleAlaPheThrProGlyHisValCysSerGluIleSerAlaIleCysProHeCys 400   |
| Db                  | 1299 TGGTGCAGATCCCCTGCTGCCACCGAACGGCACGGTTTACGGCGCTGTCCCTCTGC 1358  |
| Qy                  | 401 AlaThrGlnLeuValGlyGluGlnAsnCysLeuIlePheGlnIlyProLeuSp 420   |
| Db                  | 1359 GCCAGGCACTGGTTGGTACAGACACTGCATCAAATGATTTCAGTCCAGTGGAC 1418   |
| COMMENT             | Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 220-0015, Japan (E-mail: genome-res@bsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9316) Direct Submission   |
| FEATURES            | Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Division of Experimental Animal Research in Riken contributed to prepare mouse tissues  |
| source              | Please visit our web site for further details.<br>URL: http://fantom.gsc.riken.jp/  |
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		Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
		Direct Submission
		Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL: http://genome.gsc.riken.jp/, Tel: 01-45-503-9222, Fax: 01-45-503-9216
		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
		Retina RNA was provided by Dr. Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged. Please visit our web site for further details.
		URL: http://fantom.gsc.riken.jp/.
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		SRYACRILCDRIPPTYTAAGKMRWTFQIGERAKWRTDGLMDQGTLTGTGTTGAACTGGTGAQSTI
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		VYRCGHYHGNGCRBQGPBRECFLRQVYVUWLGOBALGICDGPSPSHATA
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	Query Match:	71.3%
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		194 CCTCTGGTGAAGAA----CACTGCAGCGAGGGCCCTCAAGTAGTCGACTCATC 247
		24 ValIleGlyIVTAspIgLyAlaLeuProAsnGlyApArgClyIATGargLysserArgPhe 43
		248 GTCTGGCTCACATGGTCTGCAGTGAGCAAGCAAGGCCCGGCCAACGCCCTG 307
		44 AlaLeuTyryllysArgProlysAlaLysGlyValysProSerThrValysValIleSer 63
		308 GCACtGAGGCCGCCCCACCACTGCGCAACGGAGTGAGCACTGTCACCTCTC 367
	US-10-041-030-4 (1-420) x AK044418 (1-1879)	
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		343 ProTyroValProLeuProIlePheGlyCysGluAlaGlyPhytyrValAspAlaGlyProPro 362
		1205 CCCTATGCCCCCTGGCTGGCTGGAGGGCCGCTCTGGCTGGACCCCTGGCCACCC 1264
		363 ThrHisAlaPheThrProCysGlyYhiValCysValGlyLysSerAlaLysTyroPhe 382
		1265 AGCCACGCTTTCGACCTCTGGCACGCTGCTGAGAGACAGCTCCCTACTGGCT 1324
		383 GluIleProLeuProIleGlyCysGluAlaGlyPhytyrValAspAlaGlyProPro 402
		1325 GAGACCCGCTGGCCGACGCCACATGCTTCAGCGTCCTGACCCCTCTGGAGCT 1384
		403 GluLeuValGlyGluGlnAlaCysIleLeuIlePheGlyGlyProIleAsp 420
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ORIGIN	ORIGIN
Alignment Scores:	Alignment Scores:
pred. No.:	pred. No.:
Length:	Length:
Score: 1620.00	Score: 1620.00
Percent Similarity: 77.0%	Percent Similarity: 77.0%
Best Local Similarity: 67.5%	Best Local Similarity: 67.5%
Query Match: 70.7%	Query Match: 70.7%
DB: 4	DB: 4
US-10-041-030-4 (1-420) x HSMB05479 (1-2710)	US-10-041-030-4 (1-420) x HSMB05479 (1-2710)
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pred. No.:	pred. No.:
Length: 2710	Length: 2710
Score: 1620.00	Score: 1620.00
Percent Similarity: 77.0%	Percent Similarity: 77.0%
Best Local Similarity: 67.5%	Best Local Similarity: 67.5%
Query Match: 70.7%	Query Match: 70.7%
DB: 4	DB: 4
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199 TCCCCGGT----GAAGATGCCAGGCCATCAAGTATGTTGAACT 252	199 TCCCCGGT----GAAGATGCCAGGCCATCAAGTATGTTGAACT 252
Qy 23 ValValLeuGly-----	Qy 23 ValValLeuGly-----
Db 27 -----TyrAsnGlyAlaLeuProAsnGlyAsparGlyArg 38	Db 27 -----TyrAsnGlyAlaLeuProAsnGlyAsparGlyArg 38
Db 313 ACTGGCCCAGGSCACAGCTGCTGCTACATGTTCTGGCAACTGGGAGGGCC 372	Db 313 ACTGGCCCAGGSCACAGCTGCTGCTACATGTTCTGGCAACTGGGAGGGCC 372
Qy 39 ArgLySerArgpheAlaLeuTyroLysArgProLysAlaAsnGlyValLysProSerThr 58	Qy 39 ArgLySerArgpheAlaLeuTyroLysArgProLysAlaAsnGlyValLysProSerThr 58
Db 373 CGGGAAAGCCGCTGGACTGGCCGGCTCGACGCCAACGGGAGAGCCT 432	Db 373 CGGGAAAGCCGCTGGACTGGCCGGCTCGACGCCAACGGGAGAGCCT 432
Qy 59 ValHisvalleSerThrProGlnAlaSerLysValLysSerCysLysGlyLysIle 78	Qy 59 ValHisvalleSerThrProGlnAlaSerLysValLysSerCysLysGlyLysIle 78
Db 433 ATGCCACATCTCACGCCGCTCGTCACGCCAGTACCGTACGACAGC 492	Db 433 ATGCCACATCTCACGCCGCTCGTCACGCCAGTACCGTACGACAGC 492
Qy 79 IleSerTyThrIleSerArgAsnGlnThrValValValGluTyRThiSibLysLys 98	Qy 79 IleSerTyThrIleSerArgAsnGlnThrValValValGluTyRThiSibLysLys 98
Db 493 ATCTCGTATACTACTGTCGGGACTCGCTCATAGCTGATACATGATAGCGC 552	Db 493 ATCTCGTATACTACTGTCGGGACTCGCTCATAGCTGATACATGATAGCGC 552
Qy 99 ThraspMetpheGlnValGlyArgSerThrGluSerProLepheAspPheValValThrasp 118	Qy 99 ThraspMetpheGlnValGlyArgSerThrGluSerProLepheAspPheValValThrasp 118
Db 553 ACAGACATGCTTCCAGATGGCCGCTCCAGAGAACATGATGCTGTCAGAC 612	Db 553 ACAGACATGCTTCCAGATGGCCGCTCCAGAGAACATGATGCTGTCAGAC 612
Qy 119 ThrIleSerGlySerGlnLysAspGluAlaGlnIleThrGlnSerThrIleSerArg 138	Qy 119 ThrIleSerGlySerGlnLysAspGluAlaGlnIleThrGlnSerThrIleSerArg 138
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ACCESSION AY408791	ACCESSION AY408791
VERSION AY408791.1	VERSION AY408791.1
GSS. SOURCE	GSS. SOURCE
ORGANISM Mus musculus (house mouse)	ORGANISM Mus musculus (house mouse)
Bukar-Yata, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	ORGANISM Mus musculus (house mouse)

REFERENCE		Sciurognathus; Muridae; Murinae; Mus.	
AUTHORS		Clark,A.G., Gianoebki,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civerello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Srinivasan,J.J., Adams,M.D. and Cargill,M.	
TITLE		inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL		Science 302 (5652), 1960-1963 (2003)	
PUBLMED		14671302	
REFERENCE		2 (bases 1 to 1242)	
AUTHORS		Clark,A.G., Gianoebki,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civerello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Srinivasan,J.J., Adams,M.D. and Cargill,M.	
TITLE		Direct Submission	
JOURNAL		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering them based on alignment.	
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Query Match:	70.4%	Indels:	7
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Db	4 CCTGGTGAA----GCACTCGCAGCGGCCATCGATGTTGACTCATC 57	Db	946 GGCAGCCGGAGGAAACAGCCCCCAGGAGGAGAGTGTCTCTGGCA 1005
Qy	24 ValLeuGlyTrpAlaGlnGlyAlaLeuProGlnGlyAspArgGlyArgGlySerArghe 43	Qy	343 ProTyroValProLeuPhePheLeuGlyCysGluAlaGlyPheTyroValAspAlaGlyPro 362
Db	58 GTCCTGGCTCACATGGGCTCTGGCACTGGAGAACGCCGCGAAGGCCGCT 117	Db	1006 CCTTATGTCGCCCTGGTGGTGGTAGGAGGCCGCTCTGGACCTGGCCACCC 1065
Qy	44 AlanLeuTyroLybArgProLysAlaAspGlyValWtysProSerThrValHisValLeuIle 63	Qy	363 ThrHisAlaPheThrProCysGlyHisValCysSerGluLysSerAlaLysTyrPhe 382
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Qy	64 ThrProGlnAlaSerLysAlaLeuSerCysLeuGlyGlnHisSerValThrIle 83	Qy	383 GluIleProLeuProHisGlyThrHisAlaPheIleAlaCysProHeCysAlaThr 402
Db	178 ACACCA-----CTGCCCTGAGTAACCCGAGCCACACATCTCATCCACTG 228	Db	1126 CAGACACCCTGCCGACGCCACCATGCTTCAGCTGCTGCCCTCTGGAGCT 1185
Qy	84 SerArgGangInthrValValGluGlyTyrThrIleAspLysAspThrAspPheGln 103	Qy	403 GluLeuValGlyGluGlnAlaCysTleLeuIlePheGlnGlyProLeuAsp 420
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ACCESSION	AK033815	DEFINITION	AK033815.1 GI:26329492
VERSION		DEFINITION	HCC; CAP trapper.
KEYWORDS		DEFINITION	Mus musculus (house mouse)
SOURCE		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Burchontodonta; Glires; Rodentia; Sciurognathus; Muridae; Murinae; Mus.
REFERENCE			
AUTHORS	Carminci,P. and Hayashizaki,Y.	1	
TITLE	High-efficiency full-length cDNA cloning	High-efficiency full-length cDNA cloning	
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
PUBLMED	10349636		
REFERENCE	2		
AUTHORS	Carminci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kouno,H., Ozaki,Y., Muramatsu,M. and Hayashizaki,Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
TITLE	164 LysineNlePhelLeuGlyLelutuValAlaLysPheAspAspCysLysMetmap 183		

JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBLISHED	11042159
REFERENCE	/db_xref="GI:26329493"
AUTHORS	/translation=RPAKIVCDNNEPYTARIFAGFDSQKNIEGAKWNRDGH
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasihagi,K., Yoneda,Y., Ishikawa,T., Ozawa,M., Ohara,E., Wakahiki,M., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE	RIKEN integrated sequence analysis (RSA) system--384-format sequencing pipeline with 344 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBLISHED	11076861
REFERENCE	/note="putative"
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	/note="putative"
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	/note="putative"
AUTHORS	(bases 1 to 2414)
6	Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanasaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirokawa,T., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kasukawa,T., Kation,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numata,R., Ohno,M., Obato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sobabe,Y., Tagami,M., Tagawa,A., Takahashi,T., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toyoda,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
COMMENT	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 220-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503 9222, Fax: 81-45-503 9216)
FEATURES	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.
source	URL: http://genome.gsc.riken.jp/.
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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
 Run on: March 2, 2006, 04:45:41 ; Search time 809 Seconds  
 (without alignments)  
 3460.038 Million cell updates/sec

Title: US-10-041-030-4

perfect score: 2290  
 Sequence: 1 MFSPGQEBHCAPNPKPVKG.....ATOLVGEONCILKIFQGPI 420

Scoring table:

BLOSUM62  
 Xgapop 10.0 , xgapext 0.5  
 Vgapop 10.0 , Vgapext 0.5  
 Fgapop 6.0 , Fgapext 7.0  
 Delop 6.0 , Delett 7.0

Searched:

4996997 BeqB, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
 Listing first 45 summaries

Command line parameters:

-MODE=frame+P2n.model -DEV=xlh  
 -Q=/abs/ABSSWEB spool/US10041030/runat\_01032006 134403 21809/app\_query.fasta\_1  
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 -UNITS=6bits -STARTR=1 -ENDR=1 -MATRIX=BLOSUM62 -TRANS=human40\_cdi -LIST=45  
 -DOCALIGN=200 -THR SCORE=SPEC -THR MAX=100 -THR MIN=0 -ALIGN=15 -MDR=LOCAL  
 -OUTFILE=pt0 -NORM=ext -HEAISIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=tabel08  
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 -NO MMAP -NRG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -KGAPRT=0.5 -FGAPOP=6 -FGAPRT=7  
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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 13: geneseqn2004bs:  
 14: geneseqn2005s:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Length	DB ID	Description	
1	2290	100.0 1565	6	AAL46323	AAL46323 Human M23	
2	2290	100.0 1823	10	ADC30209	ADC30209 Human nov	
3	2290	100.0 4553	6	ABP78319	ABP78319 Nucleotide	
4	2290	100.0	5579	8	ACC42349	ACC42349 Human Map

### RESULT 1

ID AAL46323 standard; CDNM; 1565 BP.

AC AAL46323;

DT 19-JUL-2002 (first entry)

DB Human M23 coding sequence SEQ ID NO: 15.

XN Human M23 coding sequence SEQ ID NO: 15.

NR Neurodegenerative disease; M30; M31; M32; M33; stroke;

KW fragile X syndrome; Huntington's disease; Parkinson's disease;

KW Alzheimer's disease; multiple sclerosis; ovarian cancer;

KW neurodegeneration; immune disorder; autoimmune disease; allergy;

KW infection; leukemia; inflammation; neuroprotective; cerebroprotective;

KW immunosuppressive; cytostatic; nontoxic; antiparkinsonian; antiallergic;

KW viricide; antiinflammatory; gene; ss.

OS Homo sapiens.

XN W0200221138-A2.

XX 14-MAR-2002.

XX 07-SEP-2001-2001IWO-EP010366.

XX 07-SEP-2000; 2000IUS-00657479.

### ALIGNMENTS

Abl58449 Human pel  
 Abp48670 Human pel  
 Abp48648 Murine pel  
 Abp48668 Mouse pel  
 Acc42348 Mouse MAP  
 Abl58447 Human pel  
 Abp48666 Human Pel  
 Abx05095 Human nov  
 Aal46320 Human M30  
 Aal46319 Human M30  
 Adf83102 Human Pel  
 Adp5619 Human PRO  
 Adp24928 PRO polyp  
 Ady17389 DNA encod  
 Ady20613 DNA encod  
 Aal46316 Rat M30 c  
 Abp4846 Murine pe  
 Adp46664 Mouse Pe  
 Aal46317 Human M30  
 Abp58452 Human pel  
 Adp8677 Human Pel  
 Add71199 Human int  
 Aal46322 Human M31  
 Adc39836 Human nov  
 Aal46321 Murine M3  
 Aal46318 Human M30  
 Aac66453 Human sec  
 Aah16312 Human cDN  
 Aah77808 Nucleotid  
 Adb6804 Human cDN  
 Aak94835 Human ful  
 Adl31993 Full leng  
 Abi0973 Drosophil  
 Aak73420 Human 1mm  
 Aab66590 Human cDN  
 Adc32115 Human nov  
 Aab66861 DNA encod  
 Aal46314 Human M33  
 Aal46324 Human M32  
 Aah89787 Human gen  
 Abi09072 Drosophil

PA (AXAR-) AXARON BIOSCIENCE AG.  
 XX  
 PI Schneider A, Hiemisch H, Rossner M, Klugmann M, Naim J, Spielvogel D, Scheek S;  
 XX  
 DR WPI; 2002-282287/33.  
 PT diagnosis of neurodegenerative disease comprises detecting level of M30-  
 PT family proteins.  
 XX  
 PS Claim 3, Page 113-116; 130pp; German.

XX The present invention relates to a method of diagnosing neurodegenerative  
 CC diseases, comprising determining the concentration of a protein in a body  
 sample, where the protein may be M30 or a variant thereof, M31, M32 or  
 M33. The method is used to diagnose neurodegenerative diseases,  
 CC particularly stroke but also e.g. fragile X syndrome, Huntington's,  
 Parkinson's and Alzheimer's diseases, multiple sclerosis etc. Also,  
 CC overexpression of M31 can be used for diagnosis of carcinoma and sarcoma,  
 especially ovarian cancer. The protein can be used to identify specific  
 CC ligands potentially useful for treating neurodegeneration, immune system  
 inflammation (e.g. autoimmune diseases, allergy, viral infection, leukaemia,  
 CC carcinoma and sarcoma. Inhibitors of the interaction  
 between the proteins and the protein kinase IRK-1 can be used to treat  
 CC neurodegeneration. The present sequence is a coding sequence of a protein  
 used in the method of the invention.

XX Sequence 1565 BP; 393 A; 395 C; 441 G; 336 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 7.87e-200 Length: 1565  
 Score: 2290.00 Matches: 420  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-10-041-030-4 (1-420) x AAL46323 (1-1565)

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 Db 51 ArgGTTTCCCTGCCAGGAGAACCTCGGCCCAATTAGGGCTGTAAACCG 110

QY 21 GluLeuValValLeuIleGlyTyrAspGlyAlaLeuProAsnGlyAspArgGlyArgGly 40  
 Db 111 GAGCTGGTGTCTGGGTACATGGCTTACCCATGGAGATAGGGAGA 170

QY 41 SerArgPheAlaLeuTyrAspProValLeuAlaGlyAspGlyValAspSerThrValHis 60  
 171 ATGAGATTGCCCCCTACAGGGCCCAAGGCAATGGTCACCGCTCAT 230

QY 61 ValLeuSerThrProGlnAlaSerLysAlaIleSerCysArgGlyGlnHisSerIleSer 80  
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QY 81 TyrThrLeuSerArgAspGlnThrValValValGluThrIleAspProAspThrAsp 100  
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QY 101 MetGheGlnValGlyArgSerThrGluSerProIleAspPheValThrAspThrIle 120  
 351 ArgGTTCACTGGCAGATCACAGAAAGCCCTATCGACTTCTGTCACAGATT 410

QY 121 SerGlySerGlnIleThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
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QY 161 AspSerSerLysAsnIlePheLeuIleGlyGluIleValAlaAlaLysAspProAspGly 180

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 QY 711 CGAGAACCTGGCCAGCACAGGAAGAGCTGGTGAAGTGGAGACAGCTCTG 770  
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 Db 771 CAGGACGCTCTCTCATGACCTGACCTGAGCTGTTGGGSCACTCTCTCTGGAGA 830  
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 Db 951 GAGGAGGAGGAGGAGGAGCCTGGGATATCAGTTGTCGACCGTGACGGTACAC 1010  
 Db 321 AspTRPGLYHisArgSerAspThrGluIleIleGluAlaIleAspGlnGluCysProMetCysArgThr 340  
 Db 1011 AACGGCCACGGAGGAGCAGCGGAGCCACAGGGAGGAGTGTCCATGCTGAGCT 1070  
 QY 341 ValGlyProTyroValProLeuTrpLeuIleCysGluAlaGlyPheTyrValAspAlaGly 360  
 Db 1071 GGGGCCCTATGGCCCTCTCTGGCTGCTGGCTGCTGAGGTATTGAGCCAGGAGA 1130  
 QY 351 ProProThrIleAlaProThrProCysGlyHisValCysSerGluIlysSerAlaIleTyr 380  
 Db 1131 CCCCAACTCTATGCTTCACTCTCTGAGCTGAGCTGCTCGAGAGTCTGCAAAATAC 1190  
 QY 381 TrpSerGlnIleProLeuProHisGlyThrIleAlaPheHisAlaAlaCysProPheCys 400  
 Db 1191 TGTCTCTGATCCGCTTCCTGAGCTCTGCTACGCTGCTGCTGCTTCTGT 1250  
 QY 401 AlaThrGlnIleValGlyGluGlnAspCysIleLysIleLeuIlePheGlnGlyProIleAsp 420  
 Db 1251 GCTACACGGCTGGTGGAGGAACTGCATCAATTAAATTCCAGGGTCATGAC 1310

RESULT 2  
 ADG30209 standard; cDNA; 1823 BP.  
 XX  
 AC ADC30209;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Human novel cDNA sequence, SEQ ID NO: 291.

XX Human; diagnostic; drug screening; forensics; gene mapping;  
 KW biodiversity assessment; Parkinson's disease; Alzheimer's disease;  
 KW neurodegenerative diseases; anemia; platelet disorder; wound; burns;  
 KW ulcers; osteoporosis; autoimmune disease; cancer;  
 KW molecular weight marker; food supplement; anti-parkinsonian; nootropic;  
 KW neuroprotective; anti-anemic; anti-coagulant; thrombolytic; pulmonary;  
 KW antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;  
 KW gene therapy; chromosome 14q21; gene; ss.  
 XX OS Homo sapiens.  
 XX PN W02003029271-A2.

XX 10-APR-2003.  
 PD XX  
 PP XX  
 24-SEP-2002; 2002WO-US030474.  
 XX PR 24-SEP-2001; 2001US-0324631P.  
 XX PA (HYSEB-) HYSEB INC.  
 XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T,  
 Zhou P, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;  
 PI Haley-Vicente D, Drmanac RR;  
 XX DR WPI; 2003-371981/35.  
 DR P-PSDB, ADC31180.

XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or  
 PT treating disorders such as neurodegenerative diseases, anemias, platelet  
 disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 PT cancer.

XX PS Claim 1; SEQ ID NO 291; 1185pp; English.

CC The invention relates to 971 novel human cDNA sequences (ADC2991-  
 CC ADC30809) and the polypeptides they encode (ADC0890-ADC31860). The  
 CC invention also relates to nucleic acid sequences over 99% identical with  
 the novel human cDNAs. The invention additionally encompasses expression  
 CC vectors and host cells comprising a nucleic acid of the invention; the  
 CC recombinant production of a polypeptide of the invention; an antibody  
 CC against a polypeptide of the invention; a method of detecting  
 CC polynucleotides or polypeptides of the invention; and methods of  
 identifying a compound which binds to a polypeptide of the invention. The  
 CC invention further discloses methods of preventing, treating or  
 ameliorating a medical condition; kits comprising polynucleotide probes  
 CC and/or monoclonal antibodies for carrying out the methods of the  
 invention; methods for the identification of compounds that modulate the  
 CC expression or activity of the polynucleotide and/or polypeptide; and 757  
 CC contig sequences corresponding to the cDNA sequences of the invention  
 CC (ADC3161-ADC3267) and the polypeptides encoded by the contig (ADC32028  
 CC -ADC33194). The nucleic acids and polypeptides of the invention are  
 CC useful in diagnostics, drug screening, forensics, gene mapping, in the  
 CC identification of mutations responsible for genetic disorders or other  
 CC traits, for assessing biodiversity, and in producing many other types of  
 CC data and products dependent on DNA and amino acid sequences. They are  
 CC also used for treating diseases such as Parkinson's disease, Alzheimer's  
 CC disease and other neurodegenerative diseases, anaemia, platelet  
 CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or  
 CC cancers. The nucleic acids may also be used as hybridisation probes or  
 CC primers, and in the recombinant production of a protein. The polypeptides  
 CC are also useful in generating antibodies, as molecular weight markers,  
 CC and as food supplements. The present sequence represents a specifically  
 CC claimed human cDNA sequence of the invention. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1823 BP; 425 A; 483 C; 530 G; 385 T; 0 U; 0 Other;

Alignment Scores:  
 Alignment Score: 9.59E-200  
 Score: 2.250.00 Length: 1823  
 Percent Similarity: 100.0% Matches: 420  
 Best Local Similarity: 100.0% Conservative: 0  
 Query Match: 100.0% Mismatches: 0  
 DB: 100.0% Indels: 0  
 Gaps: 0

US-10-041-030-4 (1-420) x ADC30209 (1-1823)

QY 1 MetPheSerProGlyGluGluHisCysAlaProAlaLysGluProValIleTyrLeu 20  
 Db 265 ATGTTTCCTGGCCAGGAGAACACTCGGCCCAATTAGGGCAGTAGAAATACGG 324  
 QY 21 GluLeuValValleuglyTyrAsnGlyAlaLeuProAsnGlyAspArgGlyArgGly 40

Do 325 GAGCTGGGGCTCTGGCTACATGGCTTACCCATGGAGATAGAGGGAGAA 384  
 QY 41 SerArgPheAlaLeuIrrlySargProlySalaAsnGlyVallyProSerThrValHis 60  
 Do 385 AGCTGATTCGCTCTCAAGGCCTGAAAGGCCTGAAAGTGCAACCCGCTCAT 444  
 QY 61 ValIleSerThrProGlnAlaSerLysGluAlaLysSerCysLysGlyGlnHisSerIleSer 80  
 Do 445 GTCATAATCACGCCAGCATGCTCAAGCTATAGCTGCAAGGTCAACAGTATTC 504  
 QY 81 TyrThrIleSerArgArgLnrValValGluIrrThrIleAspLysAspThrASP 100  
 Do 505 TACATGTTCTGAGGAATGAGCTGTGTTGAGTACAGCTGCAAGTCACATGATTAAGCTATCGGT 564  
 QY 101 MetPheGlnValGlyArgSerThrGluSerProLeuAspPheValValThrAspThrIle 120  
 Do 565 AspTTCGCGGCGGCACTTCAGCAAGGAAAGCCATTATGCACTGTCACAGTCACAGA 624  
 QY 121 SerGlySerGluAlaThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
 Do 625 TCTGGACACCAGACACAGGAGCAGACAGGAGCAAGCAGACAGCAGATCCAGGTCGCC 684  
 QY 141 CysArgIleValCysAspArgAsnGluIrrProThrAlaAspIlePheAlaLysGlyPhe 160  
 Do 685 TCTAGGATGCTGAGGAGGATGAACTTACACAGCAGATATTGCGCCCGATT 744  
 QY 161 AspSerSerLysAlaIlePheLeuIrrlyGluIrrlyGluIrrlyGluIrrlyGluIrrly 180  
 Do 745 GACTCTCCAAACATTTCTTGGAAAGGAAAGCAGCAAGTGGAAAACCCGAGGC 804  
 QY 201 GluGluSerGlnProGlyValIrrProGluIleSerIleCysGlyAspValThrIle 220  
 Do 865 GAGGAGTCCACCCGGGTCTGCGAGCTCTCTGAGATGTGACACCTTG 924  
 QY 221 ArgGlutnArgSerAlaLysGlnArgGlyIrrlyGluIrrlyGluIrrlyGluIrrly 240  
 Do 805 CACTGGATGGCTCTACTACTATGCTCTCTGATGCTCTGACCTAC 864  
 QY 925 CGAGAACGAGGCGCCAGGAGCTGGAAAGCTGGAAAGTGGAAAGTGGAAAGTGG 984  
 Do 241 GluAspArgIleSerLeuIleAspLeuCysGlyAlaThrIleLeuIrrPheThrAlaAspGly 260  
 Do 1045 CTTTTCTAATCTCACTCACTAGAGGACAATAGAGCCCTCCGGCAGGAAATTACGCC 1104  
 QY 985 CAGGAGCCTCCCTCATGCTGACCTGTCGGCCACTCTCTCTGGAGAACAGTGG 1044  
 Do 261 LeuPheHsIrrProTrgIrrlyGlyIrrlyIleGluIleLeuIrrGlyGluIleAsnAla 280  
 Do 1015 CTTTTCTAATCTCACTCACTAGAGGACAATAGAGCCCTCCGGCAGGAAATTACGCC 1104  
 QY 281 ArgProGlyIrrProValGlyIrrLeuIrrAlaIrrLeuIrrAlaIrrProSerIleAsnArglyGlu 300  
 Do 1105 CGCCCTCACTGCTGGGCTGACCCCTCCGGCTTCCGGAACTACCGGAG 1164  
 QY 301 ValValGluGluIrryGluIrrProTrpIleSerCysGlyIrrlyIleValHisIrrly 320  
 Do 1165 GAGGAGGAGGAGCACCCCTGGGAACTACCGGAG 1224  
 QY 321 AsnTrpGlyIrryGluIrrProTrpIleSerCysGlyIrrlyIleValHisIrrly 340  
 Do 1225 AACTTGGCCCATGGAGTGCACGGGCCACAGGAGGAGCTGCCTATGCGGAGCT 1284  
 QY 341 ValGlyProTrpIrrProLeuIrrlyCysGluAlaLysGlyPhenylTyrValAspAlaGly 360  
 Do 1205 CGGGCCCTCTGCTGGCTGAGGAGATTCAGTGTGGCCACGTCACGGTACAC 1344  
 QY 361 ProProThrIrrIleAlaIrrPheThrProCysGlyIrrValCysSerGluIrrSerAlaIrrlyTyr 380  
 Do 1345 CCCCAACTCTCATCTTCACTCCCTGAGCAGCTGCTGAGAAGTCTGCAAAATAC 1404  
 QY 381 TrpSerGlnIleIleProIrrGlyIrrIleAlaIrrAlaCysProPheCys 400

Db 1405 TGGCTCAGATCCGTTGCTCATGGAACTCATCCATTCAAGCTGCTGCCCCCTTCGT 1464  
 QY 401 AlAhrqinluuvalgylgluglnasnCysileylsaurlePheglnglyProleasp 420  
 Db 1465 GCTACACGCTGGTGGGAGCAGACTCATCATTATTTCGAGTCATTGAC 1524  
 result 3  
 ABQ78319 standard; DNA; 4563 BP.  
 XX AC ABQ78319;  
 XX DT 05-NOV-2002 (first entry)  
 XX DE Nucleotide sequence of human Pellino 2.  
 XX KW Pellino 2; cancer; Pellino 1; cancer treatment; epithelial cancer;  
 KW gastrointestinal tract cancer; gene; ss.  
 OS Homo sapiens.  
 XX FH location/Qualifiers  
 FT CDS  
 FT 5' UTR 501. 1763 /product= "Pellino 2"  
 FT /tag= b 1764. .4563  
 XX PN WO200259611-A2.  
 XX PD 01-AUG-2002.  
 XX PF 28-DEC-2001; 2001WO-US051368.  
 XX PR 02-JAN-2001; 2001US-0259502P.  
 XX PA (TULSA-) TULARIK INC.  
 XX PI Powers S, Mu D, Xiang P, Peng Y,  
 XX DR WPI; 2002-619185/66.  
 DR p-PSDB; ABBV077.  
 XX PT Detecting cancer cells in mammalian sample, useful for identifying  
 PT inhibitors for treating cancer e.g. epithelial cancer, comprises  
 PT detecting an overexpression of, or increase in copy number of genes  
 PT encoding, Pellino 1 and Pellino 2.  
 XX PS Claim 31; Page 57-61; 69pp; English.  
 CC The present sequence encodes human Pellino 2. The specification describes  
 CC a method for detecting cancer cells in biological sample from a mammal.  
 CC The method comprises detecting an overexpression of, or increase in copy  
 CC number of genes encoding, polypeptides Pellino 1 or Pellino 2. The method  
 CC is useful in detecting cancer or propensity to develop cancer, monitoring  
 CC the efficacy of cancer treatment, identifying inhibitors of Pellino 1 and  
 CC 2, inhibiting the expression and/or activity of Pellino 1 and 2 in cancer  
 CC cells, and treating cancer or inhibiting proliferation of cancer. The  
 CC cancer can be epithelial cancer, such as lung, colon, ovarian, breast,  
 CC prostate, kidney, stomach, bladder, or any cancer of the gastrointestinal  
 CC tract.  
 XX SQ Sequence 4563 BP; 1146 A; 1028 C; 1106 G; 1283 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 3.39e-199 Length: 4563  
 Score: 2290.00 Matches: 420  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 6 Indels: 0  
 Gaps: 0  
 DB: , US-10-041-030-4 (1-420) x ABQ78319 (1-4563)

WY

QY 1 Met-PheAsp-ProGlyGlnGluGluIleCysAlaProLysValProValValSerGly 20  
 Db 501 ArgPTTCGCCCTGGAGGAGAACCTGGCGCCCAATAGGAGCCAGTGAAATCGGG 560  
 QY 21 GluIleValValLeuIgLyTyrArgIlyAlaLeuProArgIlyAspArgIlyArgIly 40  
 Db 561 GAGCTGGTGGCTGGGAGTACATGGCTTACCCATGGAGATAGGGAGGGAAA 620  
 QY 41 SerArgPheAlaLeuTyrLysArgProIysAlaArgIlyVallysProSerThrValHs 60  
 Db 621 AGTGAATTGGCCCTTACAGCGGCCAGGCAATGGTCAACCCAGCACGTCCT 680  
 QY 61 ValIleSerThrProGlnAlaSerIlyValIleSerCysIlyValGlnSerIleSer 80  
 Db 681 GTCATTCACGCCAGGCATCAAAGCTTACGTCAGCTCAANGTCACAGTATTC 740  
 QY 81 TyRThrIleSerArgArgIntrValValValGlyIutyrThrHisAspIlyAspThrAsp 100  
 Db 741 TAGCTTGTCAAGGAATCAGCTGTTGGTGGAGAPACACATGATGATAGATACGGAT 800  
 QY 101 MetPheGlnValGlyAspSerIleSerProLeaspPhValValThrAspThrIle 120  
 Db 801 ATGTTCTGGTAGGCAGT 860  
 QY 121 SerDlySerGlnAlaSerIlyValIleThrGlnSerThrIleSerArgPhAla 140  
 Db 861 TCGGGCAGCCAGACAGCAGCACAGCCAGATCACAGCACAGCATTCAGGTCGCC 920  
 QY 141 CyBargIleValCysBargArgAsnGluProTyThrAlaArgIlePhAlaAlaLgyphe 160  
 Db 921 TCGAGGATGTGTCGAGAAGCTACACAGCAGGATATGCCCGGGATT 980  
 QY 151 AspSerSerIleValIlePheIleUgIlyIleUgIlyIleUgIlyIleUgIlyIleUgIly 180  
 Db 981 GACTCTCCAAACATTTCTGGAGAAAGCAGCAAGCAGGAAACCCGAGGC 1040  
 QY 181 HisMetAspGlyLeuThrThrArgIlyValLeuValMethIleProArgGlyGlyPheThr 200  
 Db 1041 CACATGGATGGGCTACTACTATGGGCCCTGGTCATGCCACGGGGCTCACC 1100  
 QY 201 GluGluLysGlnProGlyValTrpArgGluIleSerValCysGlyAspValtyThrIle 220  
 Db 1101 GAGGAGTCCAGCCGGGGCTGGCGAGCTCTCTGAGAGTGTGAGATGTGACCTTG 1160  
 QY 221 ArgGluLysArgSerAlaGlnArgIlyIleUgIlyIleUgIlyIleUgIlyIleUgIly 240  
 Db 1161 CGAGAACAGGAGGCCAGCAACGAGGAAAGCTGGGGAGATGAGCAACAGCAGGC 1220  
 QY 241 GluAspGlySerIleIleAspIleCysGlyAlaThrIleLeuIleTrpArgGly 260  
 Db 1221 CAGGAGCCCTCCCTCATGGCTGACCTGCTGGGGCACTTCTCTGGAGAACACCGATGG 1280  
 QY 261 LeupheHisthBrothGlnIlyShiIleGluIleLeuAspGlnGluIleAlaAla 280  
 Db 1281 CTTTTCACTCAACTCACTAGAGCACATAGAGCCCTCCGGCAGGAGATAACGCC 1340  
 QY 281 ArgProGlyCysProValGlyLeuAspIleLeuAlaLeProSerIleAspArgIleGlu 300  
 Db 1341 CGCCCTGGTGGCTGGGGCTCAACCCCTCCGAGCATCAAGCAGGAG 1400  
 QY 301 ValValGluGluIlyGlnProTrpIleTyrIleSerCysGlyIleValIleIlyTyrIle 320  
 Db 1401 GCGTGGGGAGAGCACCCCTGGGCTATCTCAGTGTGCGCACGTCACGGTACCAAC 1460  
 QY 321 AsnTrpGlyHisArgSerAspIleGluIleAlaAlaGluArgGluCysProMetCysArgThr 340  
 Db 1461 ACTGGGCCATCGAGGACAGCCACGAGGAGTGTCCCATGTCACGGTACCAAC 1520  
 QY 341 ValIgLyProTrpIleProLeuIlePheIlyCysGluIlyIlePheTyrValAspAlaGly 360  
 Db 1521 GAGGCGCTTATGGCCCTCTGCGCTGCTGGAGGAGGTTAGGAGCGCGAGA 1580

Qy 361 ProProThrHisAlaPheThrProGlyHisValIleSerGluLysSerAlaLysThr 380  
Db 1581 CCCCCAACATCATGTTTCACTCCCTGTGGCACCTGTCGAGAGTCGAATAAC 1640  
Oy 381 TrpSerGlnIleProLeuProHisAlaGlyThrHisAlaPheHisAlaAlaCysProHeCys 400  
Db 1641 TGGCTCTGATCTCCGGTGCTCTGACTGAACTCATTCATTTCACGGCTTGCCCTTCCTG 1700  
Qy 401 AlaThrGlnLeuValGlyGluGlnAsnValLeuIleLeuPheGlnGlyProLeuAsp 420  
Db 1701 GCTACACAGCTGGTGGGGAGCAAACTGCATCAAATTAAATTCCAGTCCAAATTGAC 1760  
**RESULT 4**  
ACC42349  
ID ACC42349 standard; cDNA; 5579 BP.  
XX AC ACC42349;  
XX DT 22-MAY-2003 (first entry)  
XX DE Human MAP kinase cascade activator #59 cDNA.  
XX KW Human; Elkl phosphorylation kinase; virucide; antiinflammatory; immunomodulator; cytostatic; antiallergic; anti-HIV; antirheumatic; antiarthritic; antiidiabetic; antiasthmatic; gene therapy; inflammation; autoimmune disease; viral disease; cancer; diabetes; rheumatoid arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis; IGA nephritis; gene; ss.  
XX OS Homo sapiens.  
XX WO2003008589-A1.  
XX PD 30-JAN-2003.  
XX PR 15-JUL-2002; 2002WO-JP007174.  
XX PR 18-JUL-2001; 2001JP-00218204.  
XX PR 31-AUG-2001; 2001JP-00263450.  
XX PR 21-JAN-2002; 2002JP-00012176.  
XX PR (ASAH ) ASAHI KASEI KOGYO KK.  
XX PI Matsuzaki O, Matsuda A, Nagano Y, Suzuki N;  
XX DR WPI; 2003-229582/22.  
XX DR P-PSDB; ABR1083.  
PR The invention relates to a novel purified protein having MAP kinase cascade effect, applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer.  
RS Claim 4; Page 631-640; 762pp; Japanese.

CC The invention relates to a novel purified protein having Elkl phosphorylation activity and/or an activity of activating Elkl phosphorylation kinase. A protein of the invention has antiinflammatory, immunomodulator, virucide, cytosatic, antiallergic, antiarthematic, antiarthritic, antidiabetic, antiasthmatic and anti-HIV activity. The polynucleotides may have a use in gene therapy. The gene and its encoded protein are applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer such as rheumatoid arthritis, diabetes; asthma, allergic rhinitis, AIDS, viral hepatitis and IGA nephritis. The present sequence is used in the exemplification of the invention

SQ Sequence 5579 BP; 1535 A; 1111 C; 1214 G; 1719 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 4.46e-199 Length: 5579  
Score: 2290.00 Matches: 420  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0

DB: Query Match: 1 100.0% Indels: 0 Gaps: 0  
US-10-041-030-4 (1-420) x ACC42349 (1-5579)  
Qy 1 MetPheSerProGlyGlnGluLysCysAlaProAsnLysGluProValLysTyro 20  
Db 177 ArgTrpTCCCTGGCAGGAGAACCTGGCCCCAAUAGGGAGCCGTTAAATCGGG 236  
Qy 21 GluLeuValValLeuGlyTrpAsnGlyAlaLeuProAsnGlyAspArgGlyArgArgGly 40  
Db 237 GAGCTGTGGTGTGGTGGGAGTGGTGTCTTACCCATGGAGATGGAGGGAGAA 296  
Qy 41 SerArgPheAlaLeuPheArgProValValAlaArgGlyValLeuProSerThrValHis 60  
Db 297 AGTAGATTGCCCTCTACAGGCCAAGGCCAAATGGTCGAACCCAGCGGCCAT 356  
Qy 61 ValLeuSerThrProGlnAlaSerIleValLeuSerCysLysGlyGlnHisSerIleSer 80  
Db 357 GTGATPATCCAGGCCAGGATTCAGGCTATCACAGGCTAACAGCTAACAGTATATCC 416  
Qy 81 TyrThrLeuSerArgGlnGlnThrValValGluTyrrThrHisAspLysAspThrAsp 100  
Db 417 TACACTTGTCAGGATCAGCTGAGTCTGTTGGTGGACTACAGCATGATAGCTACGGAT 476  
Qy 101 MetPheGlnValGlyArgSerThrGluSerProIleAspPheValThrAspProIle 120  
Db 477 ATGTTTCAGGTTGGCGAGTCAAGAGCCCTATRGACTTGTGTCAGCAGACGATT 536  
Qy 121 SerGlySerGlnAsnThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
Db 537 TCTGGCAGGCCAGAACCGGAGGAACCCCAGATCACAGGACCATATCCAGGTTGCC 596  
Qy 141 CysArgIleValCysAsnIlePheLeuGlyGlnIleAlaAlaLysAspProAspGly 160  
Db 597 TGCAAGGATCGTGTGGCACAGGATGACCTTACACGACGATATGCGCCGGATT 656  
Qy 161 AspSer-SerIysAsnIlePheLeuGlyGlnIleAlaAlaLysAspProAspGly 180  
Db 657 GACTCTTCACAAACATATTTCTGGAGAAAGGCGCAAGATGCGAAAACCCGAGGC 716  
Qy 181 HisMetAspGlyLeuThrThrAspGlyValLeuValMetHisProArgGlyGlyPhe 200  
Db 717 CACATGATGGCTACTACTAATGGCTTGGTGTGATGCCACGGAGGGCTTCACC 776  
Qy 201 GluGluSerGlnProGlyValTrpArgGluIleSerValCysGlyAspValTyrrIleu 220  
Db 777 GAGGAGTCCAGCCGGGGTTGGGGAGGACTCTGAGATGTTGAGATGTTACACTTG 836  
Qy 221 ArgGluGluArgSerAlaGlnArgGlyLysLeuValGluSerGluLysAsnValLeu 240  
Db 837 CGGAAACCCAGGTCGCCAACAGCAAGGAGAAAGCTGGTGAAGTGAGCACACGRCCTG 896  
Qy 241 GluAspGlySerLeuIleLeuPheGlyGlyAlaThrLeuLeuIleTrpArgThrAlaAspGly 260  
Db 897 CAGGAGGAGCTCCATGACTGCTGCTGAGACGCGAGATGG 956  
Qy 261 LeuPheHistDistrProArgGlyLysHisIleGluAlaIleArgGlnGluLeuAlaAla 280  
Db 957 CTTCATCACTCCACATCAAGACAGCATAGAACGCCCTCCGGAGGATTAACGCC 1016  
Qy 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlaPheProSerIleAspArgLysGlu 300  
Db 1017 CGGCCCTCAAGTCCTCTGAGCTCAACCCCTGGCTTCCACGATCAAGGAGAG 1076  
Qy 301 ValValGluGlyLysGlnProTrpAlaIleValSerCysGlyHisValHisGlyYTHis 320  
Db 1077 GTGGTGGAGGAGGAGGAGCCCTGGCCTGAGCTGAGGAGGTACAC 1136  
Qy 321 AsnTrpGlyHisSargSerAspThrGluIalaGluIargGluCysProMetCysArgThr 340  
Db 1137 ACTGGGGCCATCGGGAGTGAACGGAGGGCCACAGAGGGGGTGTCCCATGTGAGGAG 1196

341 ValGlyProTyroValProLeuTrpLeuGlyCysGluAlaLysPheTyrvAlaAspAlaGly 360  
 CC Pathways. Pellino polypeptides and polynucleotides are useful to identify  
 CC small molecule inhibitors of protein association or function of Pellino,  
 CC and other molecules involved in interleukin (IL)-1 signaling. The present  
 XX sequence represents a human pellino-2 polypeptide coding sequence  
 SQ Sequence 1263 BP; 317 A; 336 C; 351 G; 259 T; 0 U; 0 Other;  
 Db  
 Qy 381 TrpSerGlnIleProLeuProHisGlyThrHisAlaPheHisAlaAlaCysProPheCys 400  
 CC 1197 GTGGGCCCTATGTGCCTCTGGCTGGCTGGAGGTTAGTAGACCGGGA 1256  
 Db 1361 ProProThrHisAlaPheThrProCysGlyLysValCysSerGluLysSerAlaLeuTyr 380  
 CC 1257 CGCCCACTCTTGCTTCACTCCTCTGGAGAACGCTGCTGGAGTCGACAAATAC 1316  
 Db 401 AlaThrGlnLeuValGlyGluGlnAsnGlyLeuIleLeuIlePheGlyGlyProLeuAsp 420  
 CC 1317 TGGCTCTAGATCCGCTGCTCATGGACTCATGCTACGCTACTTGCCCTCTGT 1376  
 Qy 401 AlaThrGlnLeuValGlyGluGlnAsnGlyLeuIleLeuIlePheGlyGlyProLeuAsp 420  
 CC 1377 GCTAACAGCTGGTGGGAGCAAATGCAATAATTCCAGGCCAATGAC 1436

RESULT 5

ABL8449 ABL8449 standard; DNA; 1263 BP.

ID ABL8449; AC XX  
 AC ABL8449; AC XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DR Human pellino-2 polypeptide coding sequence.  
 XX  
 KW Nuclear factor-kappaB; NF-kappaB; p38; pellino; interleukin-1; viricide; anti-bacterial; fungicide; protozoicide; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antiatherosclerotic; neuroprotective; nootropic; antiluler; human; pellino-2; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PH Location/Qualifiers  
 FT 1. 1263  
 FT /\*tag= ^  
 PT /product= "pellino-2"  
 PN WO2001837339-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PR 27-APR-2001; 2001WO-US013676.  
 XX  
 PR 28-APR-2000; 2000US-0200198P.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 PI Bird TA, Cosman DJ;  
 XX  
 DR WPI; 2002-066532/09.  
 DR P-PSB; ABB07932.  
 XX  
 PT New pellino polypeptides for identifying compounds that alter polypeptide activity, treating pathogenic infection or inhibiting apoptosis, are capable of stimulating nuclear factor-kappaB- or p38-dependent transcription.  
 XX  
 PS Claim 3; Page 61; 70pp; English.

CC The invention provides polypeptides capable of stimulating nuclear factor (NF-)  
 CC kappaB-dependent transcription or p38-dependent transcription, referred as pellino polypeptides. The pellino polypeptides are useful for identifying modulators that alter the pellino polypeptide and pellino dominant-negative activity. They are also useful for identifying compounds that inhibit the binding activity of the polypeptides and to study cell-signal transduction. They are useful for preventing or treating infection by a pathogen such as virus, bacterial, fungi, algae or protozoa, or inhibiting apoptosis. Dominant-negative pellino polypeptides are useful for treating inflammatory conditions such as asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis and Alzheimer's disease, and also for inhibiting mitogen activated protein (MAP) kinase-activated

Db  
 Qy 1 MatPhoSerProGlyGnglGluHisCysAlaProAlaAspAlaGluProAlaValPheTyrGly 20  
 CC 1 ANGTTTTCCTCTGGCCAGGAGAACACTGCCCCATAGAGGAGCCATGAAATACGG 60  
 Db 21 GluLeuValValLeuGlyTyrArgGlyValLeuProArgGlyYaspArgGlyArgGly 40  
 CC 61 ValLeuSerThrProGlnAlaSerIleSerCysLysGlyGlyGlnHisSerIleSer 80  
 CC 181 GAGATATCCACGCCCTGGGCCAGGCAAGCTAACAGCTGCAAGGTCAACAGTATCC 240  
 Qy 81 TyrThrIleSerArgGlnGlyArgSerIleSerHgUserProLeuAspPheValValThrAspThrIle 100  
 CC 301 ANGTTTTCCTCTGGCCAGGAGAACACTGCCCCATAGAGGAGCCATGAAATACGG 360  
 Db 121 SerGlySerGlnGlnAsnThrAspGlnAlaGlnIleThrIleSerThrIleSerArgPheAla 140  
 CC 361 TCTGGCAGGCCAGAACGGACAAGCCAGAACGACAGCACAGACAGCACACCACTTCCGGTGGCC 420  
 Qy 141 CysArgIleValCysAspArgGluProTyrThrIlaAagileheAlaAlaGlyPhe 160  
 CC 421 TCCAGGATCGTGTGCGACAGGATGACCTACAGCACGACCGATATGGCCGGCAATT 480  
 Qy 161 AspSerIleAsnIlePheLeuGlyLeuIleAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 180  
 CC 481 GACTCTTCCAAACAAACATTTCTGGGAAAGGACCAAGTGGAAAACCCGGACGG 540  
 Db 181 HisMetAspArgPheLeuThrAspGlyLeuValAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 200  
 CC 541 CACATGAGTGAAGCTACTACTATGGCTCTGGTGTGATGTCACAGGAGACTTAC 600  
 Qy 201 GluGluUserGlnProGlyValTrpArgGlutIleSerValCysGlyAspValTyrIle 220  
 CC 601 GAGGAGTCCGCCAGCCCGGGTCTGGCCGAGATCTCTGGAGATGTGTCACCTTG 660  
 Qy 221 ArgGluLysArgSerAlaGlnIleArgGlyValLeuValGluUserGluLysAlaValLeu 240  
 CC 661 CGAAGAACGAGCTGGCCGAGGAGCTGGAGAATGGACCAAGCAGCTG 720  
 Qy 241 GluAspGlySerLeuIleAspIleCysGlyValIleLeuLeuTrpArgThrAlaAlaPhe 260  
 CC 721 CAGGAGCCTCCTCATGCTGCTGGGCCACTCTCCCTCTGGAGAAGCAGCAGTGG 780  
 Qy 261 LeuPheHisIleProThrGlyLysValLeuIleLeuIleLeuGlyGluLeuAlaAla 280  
 CC 781 CTTTTCATCTCCAACTCACAGCACATAGGCCCTCCGAGGATTAACGCCGCC 840

281 ArgProGlnGlyProValGlyLeuSerThrLeuAlaPheProSerIleSerArgGlyGlu 300  
 PT Identifying inhibitors of IL-1 signaling, useful for treating e.g.,  
 841 CGCCCTCAAGTGTCTGTCGGCTCACACCTGCTCCACATCAAGAAG 900  
 PT asthma, and rheumatoid arthritis, comprises assaying the association of a  
 Db polypeptide with IRAK-4 in the presence of a test compound.  
 301 ValValGluGluLysGlnProProAlaTyrLeuSerCysGlyHisValHisGlyThrHis 320  
 PT Pellino-1 polypeptide with IRAK-4 in the presence of a test compound.  
 Ps Claim 9; SEQ ID NO 7; 81pp; English.  
 XX  
 901 GCGGAGGAGGAGAACGGCTGGCATCTCTGTTGCGGAGTGACGGTACAC 960  
 CC The present invention describes a method for identifying compounds (C) that inhibit nuclear factor kappa B (NF- $\kappa$ B)-dependent transcription or p38-dependent transcription. The method comprises: (1) mixing a test compound with a Pellino-1 polypeptide; (2) assaying the association of the Pellino-1 polypeptide with IL-1 receptor-associated kinase 4 (IRAK-4) in the presence of the test compound; and (3) determining whether the test compound inhibits the association of the Pellino-1 polypeptide with a binding partner. Also described: (1) an inhibitory nucleic acid that binds to a nucleic acid encoding an amino acid sequence as described above, where the presence of the inhibitory nucleic acid within a cell inhibits the association of Pellino-1 with IRAK-4; and (2) an inhibitory polypeptide comprising an antibody fragment that binds to a polypeptide comprising an amino acid sequence as described above, where the presence of the inhibitory polypeptide within a cell inhibits the association of Pellino-1 with IRAK-4. (C) have antiarteriosclerotic, antiarthritic, antiasthmatic, antiinflammatory, antirheumatic, antidiabetic, gastrointestinal, neuroprotective and nontropic activities, and can be used as an IL-1 antagonist, IRAK protein kinase family inhibitor, and NF kappa B inducing kinase inhibitor. The methods and compositions of the present invention are useful for the prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the Pellino-1 polypeptide, such as asthma, rheumatoid arthritis, atherosclerosis and Alzheimer's disease. The present sequence encodes human Pellino-2, which is used in the exemplification of the present invention. The human Pellino-2 gene is located on chromosome 14, more specifically to 14q24.3.  
 CC  
 RESULT 6  
 ADP48670 standard; cDNA; 1263 BP.  
 ID ADP48670;  
 AC AC  
 XX DT 09-SEP-2004 (first entry)  
 DE Human Pellino-2 encoding cDNA SEQ ID NO:7.  
 XX  
 KW nuclear factor kappa B dependent transcription inhibitor;  
 KW NF- $\kappa$ B-dependent transcription inhibitor;  
 KW p38-dependent transcription inhibitor; Pellino-1;  
 KW interleukin 1 receptor-associated kinase 4;  
 KW IL-1 receptor-associated kinase 4; IRAK-4; antiarteriosclerotic;  
 KW antiarthritic; antiasthmatic; antiinflammatory; antirheumatic; antiulcer;  
 KW gastrointestinal; neuroprotective; nontropic; IL-1 antagonist;  
 KW IRAK protein kinase family inhibitor;  
 KW NF kappa B inducing kinase inhibitor; asthma; rheumatoid arthritis;  
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW atherosclerosis; Alzheimer's disease; human; Pellino-2; chromosome 14;  
 KW gene; ss.  
 XX OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 1. .123  
 FT /tag= a  
 FT /product= "pellino-2"  
 PN WO2004053092-A2.  
 PD 24-JUN-2004.  
 PP 09-DEC-2003; 2003W0-US039188.  
 XX 11-DEC-2002; 2002US-00317250.  
 PR (IMMUNEX ) IMMUNEX CORP.  
 PA (CLEV- ) CLEVELAND CLINIC FOUND.  
 XX Bird TA, Cozman DJ, Li X;  
 XX WPI; 2004-480927/45.  
 DR P-PDB; ADP48671.  
 QY  
 321 AsnTrpGlyHisArgSerAspThrGluAlaAsnGluCysProMetCysArgThr 340  
 961 AACGGGCCATCAGGTCACGGCCAAAGGAGGACTGCGCCATGCGGACT 1020  
 341 ValGlyProTyrosylProLeuProTyrLeuSerCysGlyHisValAlaPhe 360  
 1021 GTCGGCCCTATGTCCTCTGCTGCTGGCATCTCTGTTGCGGAGTGAC 1080  
 361 ProProThrHisAlaPheThrProCysGlyHisValCysSerAlaLysTyr 380  
 381 TrpSerGlnLeuProLeuProHisGlyThrHisAlaPheHisAlaLysCysProPheCys 400  
 1141 TGGCTCTGATCCCGTTGCCTCAGGAACATGATGATTACGGCTTGCCCTTCCTCTG 1200  
 QY 401 AlaThrGlnLeuValGlyGluGlnAsnGlyLeuLeuPheGlyGlyProLeuAsp 420  
 DB 1201 GCTACACAGCTGGGGAGCAAACTCCATCAATTTCAGCTCCATTGAC 1260

Db	361	TCTGGCAGCCAGAACGACGAGAAGCCAGATCACAGAGCACCATTCAGGTGC	420	OS	Mus musculus.
QY	141	CYBarglevalCysAsparArgAspGluProTyrrhlaargilephealaaglyphe	160	XX	
DB	421	TGCGGATGTTGCGACGGAAATGACTTACAGACGGATATTGCCGCCGGATT	480	FH	
QY	161	AspSerSerlysAlnileheleuglygluyslaalalytlylysAlnProaspGly	180	FT	
DB	481	GACTCTCCAAAACATAATTCTTGAGTAAGGCAAGCAAGTGAAACCCGACSG	540	FT	
QY	181	HisMetAspGlyLeuThrThrAsnGlyValLeuValMetHisProargGlyYpther	200	PN	WO200183739-A2.
DB	601	GAGGAATGCCAGCCGGGGCTGGCGAGATCTGTCMGTGGAGATGTACCTTG	660	XX	08-NOV-2001.
QY	221	ArgLuthargserAlaLglnGlnArgGlyLysLeuvalGluSrgLuthrasValleu	240	PR	27-APR-2001; 2001WO-US013676.
DB	661	CGAGAAACAGCTGGCCAGCAAGGAGAAAGTGGGAAGTGACCAAGTCC	720	XX	
QY	241	GlnAspGlySerLeuileLeuPleuVysGlyAlaThrLeuLeutTargThraIaaspGly	780	DR	WPI; 2002-06532/09.
DB	721	CAGGAGGGCTCCCTCATGACCTCTGAGGCCCCTCCGGCAGAGATTAACCCG	840	XX	P-PSDB; AB07921.
QY	261	LeuPheHiIthrProthrGlnVysHiIlegluLalaLeuArgGlnGlnLaleamala	280	PS	
DB	781	CTTCTCATCTCACTCCACTCTGAGACACATAGAGACCCCTCCGGCAGAGATTAACCCG	840	XX	
QY	281	ArgProGlnGlyProValGlyLeuasnThrLeuLalaPhiProSerIleasnArgyGlu	300	CC	The invention provides polypeptides capable of stimulating nuclear factor
DB	841	CGGCTCTAGTCGCTGCTGCTGGCTCACACTCTGCTCTCCAGCTCACAGAG	900	CC	(NF)-kappaB-dependent transcription or p38-dependent transcription,
QY	301	ValValGluGluLysGlnProTrrPattyLeuSerCysGlyHiIvalHiGlyYrhis	320	CC	referred as Pellino polypeptides. The pellino polypeptides are useful for
DB	901	GRGGGGAGGAGAGCAGCCTGCGGCAATCTCTGTTGGCAGGTGACGGTAC	960	CC	identifying modulators that alter the pellino polypeptide and pellino
QY	321	AspTrpGlyHiIargSerAspPheThrGluLalaAsnGluArgGluCysProMetCysArgThr	340	CC	dominant-negative activity. They are also useful for identifying
DB	961	AACGGGSCCATCGAGTCACCGAGSCAACGGAGGGAGGTCTCCATGTGCGAGCT	1020	CC	compounds that inhibit the binding activity of the polypeptides and to
QY	341	ValGlyProTrpValProleuTrpLeuGlyCysGluLalaGlyPhyThrValAspAlaGly	360	CC	study cell-signal transduction. They are useful for preventing or
DB	1021	GTGGGCCCTATGCCCTCTGACTGCTGAGGGCAGGATTATGAGCCAGGA	1080	CC	treating infection by a pathogen such as virus, bacterial, fungi, algae
QY	361	ProProThrHiIaPheThrProCysGlyHiIvalCysSerGlyIvalSerAlaIaaspTyr	380	CC	or protozoa, or inhibiting apoptosis. Dominant-negative Pellino
DB	1081	CCGCCAACTCTATGCCCTCTGACTGCCCTGCTGACCGTGTGCGAAATAC	1140	CC	polypeptides are useful for treating inflammatory condition such as
QY	381	TRPSerGlnIleProLeuProHiGlyThrHiSalApheHiSalalaCysProHeCys	400	CC	asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's
DB	1141	TGGTCTCAGATCCGCTGCTGACTGACTCATCTTACGTTGCTGCTGCCCTCTG	1200	CC	disease, ulcerative colitis, atherosclerosis and Alzheimer's disease, and
QY	401	AlaThrGlnLeuValGlyGluGlnLalaCysLeuIleLeuPheGlnIlyProLeasp	420	CC	also for inhibiting mitogen activated protein (MAP) kinase-activated
DB	1201	GCTACACAGCTGGTGGGGAGCAGACTGCAATCATATTATTCAGGTCCATTGAC	1260	CC	pathways. Pellino polypeptides and polynucleotides are useful to identify
RESULT 7				CC	small molecule inhibitors of protein association or function of Pellino,
ABLS8448				CC	and other molecules involved in interleukin (IL)-1 signaling. The present
ID	ABLS8448 standard; DNA:	1260 BP.		CC	sequence represents a murine pellino-2 polypeptide coding sequence
XX				XX	
AC	ABLS8448;				
DT	30-JUL-2002 (first entry)				
DE	Murine pellino-2 coding sequence.				
XX					
KW	Nuclear factor-kappaB; NF-kappaB; p38; pellino; interleukin-1; virucide; antibacterial; fungicide; protoacide; antiasthmatic; antirheumatic; antiarthritic; antiflammatory; antitherosclerotic; neuroprotective; nootropic; antiulcer; mouse; pellino-2; gene; ds.				

Db 181 ATGGCTCCACACCAAGCGTCCAAAGGCCAACAGCTCCAGGACATCACCATATCG 240  
 Qy 81 TyrrhleuseArgAsnGlnmrvalvalvalgluTyrrhleisAspLysAspThrAsp 100  
 Db 241 TACCGTTGTGTCAGGAGCCAGCGTAGGTTGAGTACACAGATAAACGAC 300  
 Qy 101 MetPheGlnValGlyArgSerThrGluserProleaspPheValValthrAspThrile 120  
 Db 301 AcGttttcagggttcggccacgcgttacggatcacggatccatggatccatggatcc 360  
 Qy 121 SerGlySerGluAsnThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPhenla 140  
 Db 361 TCCGGGCGGTCAGACAGAAGAT---GCCAGATCAACAGAGACCCATTGCTGTCAGCAGACGG 417  
 Qy 141 CysArgGluLeuQsAspArgAngluLysLysGluTyrrhleAlaArgIlePheAlaAlaGlyphe 160  
 Db 418 TGCGGAGCTGTGCTGAGAGGAGGAGSCATATACACGAGATATTGCGGCGAGGATC 477  
 Qy 161 AspSerSerLysAsnIlePheLeuGlyGluLysAlaAlaLysTrpIleAsnProAspGly 180  
 Db 478 GATCTTCAAATAATCTCTTGAGAGAAGCAGGAAAGCAGAAATGGAAACCTGANGGA 537  
 Qy 181 HisMetAspGlyIleThrThrAsnGlyValLeuValMethIleProArgGlyIlyPheThr 200  
 Db 538 CAACTGGATGGGACTCACTACCACTGGTGTGCTAGTGTGATGACCGCAGGAGCTTAC 597  
 Qy 201 GluGluLysArgLysGlyValTPArgLysIleSerValCysGlyAspValTyrrhle 220  
 Db 598 GAGGAATCCCAACCTGGAGCTGAGATCTGCTGTTGGATGTGGGATGTGACACCTG 657  
 Qy 221 ArgGlutThrArgSerAlaGlnGlnLysLeuValGlySerGluThrAsnValLeu 240  
 Db 658 CGAGAGACGACGAGTGGCCAGAGGAGGAAAGCTGGGAGAAAGTGACCAAGCTG 717  
 Qy 241 GluAspGlySerLeuIleAspLeuCysGlyIlyIalathrLeuLeuTPArgThrIlaAspGly 260  
 Db 718 CAAAGCCGACTCTCTCATGGCTCTGAGGACATAGAACAGCCCTTCGGCAGGAGATCGAGCC 777  
 Qy 261 LeuPheIleIleProThrGluLysIleGluAlaLeuArgLysLysIleLeuAlala 280  
 Db 778 CTGTTTCAGCTCTACTCTGAGGACATAGAACAGCCCTTCGGCAGGAGATCGAGCC 837  
 Qy 281 AspProGlyCysProValGlyIleLeuAsnThrLeuAlaPheProSerIleAsnArgGlu 300  
 Db 838 CAACCCCTGTCGCCGTCGGCCCTAACCCCTGGCTTCCCACCAACCGAGAA 897  
 Qy 301 ValValGluGlyIleGlyIleProIlePheIleAspCysGlyIlyIleValHisIlyTyrrh 320  
 Db 898 GCTGTGGAAAGAGAGACGCCCTGGCATACCTGCTGGCATGTCACCTACAC 957  
 Qy 321 AsnTrpGlyIleIleAspIleAspIleGluLysGlyCysProMetCysArgThr 340  
 Db :::::  
 Qy 958 ACTGGGACCATGGAGCAGCCGGAACCAAAGAGAGGGAGTCCATGGCAGGACT 1017  
 Qy 341 ValGlyProIleValProleaspProIleGlyCysGluLysIleIlePheTyrrValAspAlaGly 360  
 Db 1018 GGGGCCTTAATGTCCTCTCTGGCTGGCTGGATTATGTCGAGGGAA 1077  
 Qy 361 ProProThrHiaIlaPheThrProCysGlyIlyIleValCysSerIleLysSerIleValThr 380  
 Db 1078 CCCCAACTCACTCTTACCTCTGGCTGGCTGGCTGGATTATGTCGAGGGAA 1137  
 Qy 381 TpserGlnIleIleProIleProIleGlyIlyIleValPheIleAlaCysProPheCys 400  
 Db 1138 TCTGGAGATCCCACTGGCCAGGAGGACGGCTGGCTGGCTGGCTGGCTGG 1197  
 Qy 401 AlaIleArgIleLeuValGlyCysIleLysIleIlePheGlyProleasp 420  
 Db 1198 GCGACGGAGCTGTTGTCAGAACTGCAATGATTTCCAGGTCAAGTCAGTGAC 1257  
 RESULT 8  
 ID ADP48668 standard; cdna; 1260 BP.

XX  
 AC ADP48668;  
 XX 09-SEP-2004 (first entry)  
 DT  
 DB Mouse Pellino-2 encoding cDNA SEQ ID NO:5.  
 XX  
 KW nuclear factor kappa B dependent transcription inhibitor;  
 KW NF-kB-dependent transcription inhibitor; Pellino-1;  
 KW p38-dependent transcription inhibitor; Pellino-1;  
 KW interlukin 1 receptor-associated kinase 4; IL-1 receptor-associated kinase 4; IRAK-4; antiarteriosclerotic;  
 KW antiarrhythmic; antiasthmatic; antimicrobial; antirheumatic; antiulcer;  
 KW gastrointestinal; neuroprotective; nontropic; IL-1 antagonist;  
 KW IRAK protein kinase family inhibitor; asthma; inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW kappa B inducing kinase inhibitor; inflammatory bowel disease; Crohn's disease; mouse; Pellino-2; gene, ss.  
 KW atherosclerosis; Alzheimer's disease; mouse; Pellino-2; gene, ss.  
 OS  
 Mus musculus.  
 XX  
 FH Key  
 FT CDS  
 FT /product= "Pellino-2"  
 FT  
 XX WO2004053092-A2.  
 PN  
 XX 09-DEC-2003; 2003WO-US039188.  
 PR  
 XX 11-DEC-2002; 2002US-00317250.  
 PA  
 (IMMUNEX CORP.  
 PA (CLEV.) CLEVELAND CLINIC FOUND.  
 PA  
 XX Bird TA, Cosman DJ, Li X,  
 PR DR  
 DR P-PSDB; ADP48669.  
 XX  
 PR identifying inhibitors of IL-1 signaling, useful for treating e.g.,  
 PR asthma, and rheumatoid arthritis, comprises assaying the association of a  
 PT test compound with IRAK-4 in the presence of a test compound.  
 PT  
 Pellino-1 polypeptide with IRAK-4 in the presence of a test compound.  
 XX  
 PS Example 1: SEQ ID NO 5; 81P; English.  
 XX  
 CC The present invention describes a method for identifying compounds (C)  
 CC that inhibit nuclear factor kappa B (NF- $\kappa$ B)-dependent transcription or  
 CC compound with a Pellino-1 polypeptide; (b) assaying the association of  
 CC the Pellino-1 polypeptide with IL-1 receptor-associated kinase 4 (IRAK-4)  
 CC in the presence of the test compound; and (c) determining whether the  
 CC test compound inhibits the association of the Pellino-1 polypeptide with  
 CC a binding partner. Also described: (1) an inhibitory nucleic acid that  
 CC binds to a nucleic acid encoding an amino acid sequence as described  
 above, where the presence of the inhibitory nucleic acid within a cell  
 CC inhibits the association of Pellino-1 with IRAK-4; and (2) an inhibitory  
 CC polypeptide comprising an antibody fragment that binds to a polypeptide  
 CC comprising an amino acid sequence as described above, where the presence  
 CC of the inhibitory polypeptide within a cell inhibits the association of  
 CC Pellino-1 with IRAK-4. (C) have antiarteriosclerotic, antiarrhythmic,  
 CC antiasthmatic, antiinflammatory, antirheumatic, antiulcer,  
 CC gastrointestinal, neuroprotective and nontropic activities, and can be  
 CC used as an IL-1 antagonist, IRAK protein kinase family inhibitor, and NF  
 CC kappa B inducing kinase inhibitor. The methods and compositions of the  
 CC present invention are useful for the prevention and/or treatment of  
 CC diseases or conditions associated with aberrant expression or activity of  
 CC the Pellino-1 polypeptide, such as asthma, rheumatoid arthritis,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC atherosclerosis and Alzheimer's disease. The present sequence encodes  
 CC mouse Pellino-2, which is used in the exemplification of the present

XX	Sequence 1260 BP; 309 A; 357 C; 359 G; 235 T; 0 U; 0 other;	QY	301 ValValGluGluLysGlnProTyrAlaTyrLeuSerCysGlyIleGluHisGlyTyrIle 320
Pred. No. :	1.83e-189	Length:	1260
Score:	2175.50	Matches:	399
Percent Similarity:	97.4%	Conservative:	10
Best Local Similarity:	95.0%	Mismatches:	10
Query Match:	95.0%	Indels:	1
DB:	12	Gaps:	1
US-10-041-030-4 (1-420) x ADP48668 (1-1260)			
QY	1 MetPheSer-ProGlyGlnGluGluLysCysAlaProAsnLysGluProAlaProValLeuSerCysGlyIleGluGluLys 20	QY	321 AsnTrpGlyIleIleSerSerAspThrGluAlaLanGluArgGluCysProMetCysArgThr 340
Db	1 ATGTTTCGGCGGCCAGGAGAACCCAGGGCCCCAACAGAGCCGCGTGAAATACGGG 60	QY	958 AsnTrpGlyIleIleSerSerAspThrGluAlaLanGluArgGluCysProMetCysArgThr 1017
QY	21 GluLeuValValLeuGlyTyrAspGlyAlaLeuProAspGlyAspArgGlyArgGly 40	QY	341 ValGlyProTrpValProLeuTrpLeuGlyCysGluAlaGlyPhyPheTyrValAspAlaGly 360
Db	61 GAGCTGTTGGTCCCTGGGTACAATGTCGTTTACCTAATGTCGAGCAGGGCAGGGAA 120	QY	1018 GGGGCCCCCTAACGCTCTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGGA 1077
QY	41 SerGlyPhaAlaLeuTyRlySarGlyProLyBalanGlyValLeuBProSerThrValHis 60	QY	361 ProProThrIleAlaPheThrProCysGlyIleValCysSerGlyLysSerAlaLysTyr 380
Db	121 AGCGAGTTGCCCTCTTAAAGGAGCTTACGCCAGCTTACGCCAGTCACACCAAC 180	Db	1078 CCCCAACTCAGCTGGCTTCACCCCTGGGAAACGCTGTTCTAGAAAGTCTGCCAAGTAC 1137
QY	61 ValIleSerThrProGlnIaLserylAspSerCysLysGlyValIleSerIleSer 80	QY	381 TrpSerGlnIleProLeuProHisGlyIleThrAlaPheHisAlaAlaCysProPheCys 400
Db	181 ATGGCTCCAAACACCAGGGTCAAGGCATCACTCTCCAGAGCATCACAGTATCG 240	Db	1138 TGGTCAAGATCCACTGCCCACGGAAACGGCCTTCTGCCCCCTGTCGTCGTCG 1197
QY	81 TyrThrLeserArgAsnGlnIhrValValValGluTyRhrHisAspIysAspThrAsp 100	QY	401 AlaThrGlnLeuValLeuGlyGluGlnIaCysLeuLeuIlePheGlnGlyProIleAsp 420
Db	241 TACAGCTGTCACGCCAGCAGCCAGCTAGTGTGGTACACAGCATATAAGACGGAC 300	Db	1198 GCCACCGCAGCTGGTGGTGAACAGAACTGCTCAAAATTGATTTCCAGGTCCAGNGAC 1257
QY	101 MetPheGlnValGlyArgSerThrGluSer-ProIleAspPheValValThrAspThrIle 120	RESULT 9	
Db	301 ATGTTCACTGGGAGGAGGAGGAGGAAAGCCCATGACTGCTGCGTCAAGACGGAC 360	ACC42348	
QY	121 SerGlySerGlnAsnThrAspGluLysGluGlnIleThrGluSerThrIleSerArgHeAla 140	ID ACC42348 standard; cDNA; 1717 BP.	
Db	361 TCCGGGGTCAGAAAGAAT--GCCAGATCACAGACGACCATCTCTAGGTCGCA 417	XX	
QY	141 CysArgIleValCysAspPheGluProTyRhrIleArgIlePheAlaAlaLysPhe 160	AC	
Db	418 TCCAGGATCCTGTCGAGCAGAACGCCATAACAGACGCAATTTCGGGCAAGATTC 477	DT	
QY	161 AspSerSerIysAsnIlePheLeuGlyGluLysAlaAlaLysIlePheAsnProIleGly 180	XX	
Db	478 GATTTCTCCAAATTAATCTTCTCTGAGAGAGAAATGAAACCTCTGATGGA 537	DE	
QY	181 HisMetAspGlyIleIleThrThrAspGlyIleValLeuValMetHisProArgGlyGlyIleThr 200	XX	
Db	538 CACAGTGGATGACTACTAACATGCTGTCAGTAGATGCAACCCGAAAGGGCTTCACC 597	XX	
QY	201 GluGluSerIleProGlyValPheArgGluLeuSerValCysGlyAspAlaIleThrLeu 220	PR	
Db	598 GAGGRATCCGAGCTGAGCTGAGGAGATCTCTGCTCTGGAGATGTCACCTG 657	PR	18-JUL-2001; 2001JP-00218204.
QY	221 ArgGluIleArgSerAlaGlnGlyIleLeuValGluSerGluThrAsnValLeu 240	PR	31-AUG-2001; 2001JP-00263450.
Db	658 CGAGGAGACCGAGTCCGCCAGAGGGAAAGCTGTTGGAAAGGTGACCAACCTCTG 717	PR	21-JAN-2002; 2002JP-00012176.
QY	261 LeuPheIleThrProThrGlyIleIleIleLeuIleArgGluGluLeuAlaAla 280	PA	(ASAH ) ASAHI KASEI KOGYO KK.
Db	778 CTTTTCTACCTCTTCACTCGAGAACATAGAAGGCTCCGGAGAGATCACTGCC 837	XX	
QY	718 CAAGCGGCGCTCTTGTGACCTGCTGGCCACATCTCTCTGAGACGGCAGATGCC 777	PT	
Db	838 CGACCCCAAGTCCCTGGGCTTAAACCTGGCTTCCCAAGGATCAACCCGGAGGA 897	CC	
QY	241 GluAspGlySerIleLeuIleAspLeuGlyGluGluIleValIleLeuLeuIleArgGluAla 260	CC	
Db	281 ArgProGlnCysProValGlyLeuIleThrIleAlaPheProSerIleAspArgIleGlu 300	CC	
QY	838 CGACCCCAAGTCCCTGGGCTTAAACCTGGCTTCCCAAGGATCAACCCGGAGGA 897	CC	
Db		CC	
QY	The invention relates to a novel purified protein having EtkI phosphorylation-associated gene and its encoded protein with MAP kinase cascade effect, applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer.	CC	
Db	Claim 4; Page 623-627; 762pp; Japanese.	PS	
XX	EtkI phosphorylation-associated gene and its encoded protein with MAP kinase cascade effect, applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer.	XX	
XX	The invention relates to a novel purified protein having EtkI phosphorylation activity and/or an activity of activating EtkI phosphorylation kinase. A protein of the invention has antiinflammatory, immunomodulator, vasoactive, cytoprotective, antiallergic, antirheumatic, antiarthritic, antiplatelet, antiasthmatic, and anti-HIV activities. The polynucleotides may have a use in gene therapy. The gene and its encoded	XX	



Page 12

The invention provides polypeptides capable of stimulating nuclear factor (NF- $\kappa$ B)-dependent transcription or P38-dependent transcription, referred as Pellino polypeptides. The Pellino polypeptides are useful for identifying modulators that alter the pellino polypeptide and pellino dominant-negative activity. They are also useful for identifying compounds that inhibit the binding activity of the polypeptides and to study cell-signal transduction. They are useful for preventing or treating infection by a pathogen such as virus, bacterial, fungi, algae or protozoa, or inhibiting apoptosis. Dominant-negative Pellino polypeptides are useful for treating inflammatory conditions such as asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis and Alzheimer's disease, and also for inhibiting mitogen activated protein (MAP) kinase-activated pathways. Pellino polypeptides and polynucleotides are useful to identify small molecule inhibitors of protein association or function of Pellino, and other molecules involved in interleukin (IL)-1 signaling. The present sequence represents a human pellino-1 polypeptide coding sequence.

**Assignment Score:** 9.05e-166    **Length:** 1257  
**Pred. No.:** 1917.00    **Matches:** 342  
**Score:** 90.5%    **Conservative:** 38  
**Percent Similarity:** 90.5%    **Mismatches:** 38  
**Best Local Similarity:** 81.4%    **Indels:** 2  
**Query Match:** 83.7%    **Gaps:** 1  
**DB:** 6

US-10-041-030-4 (1-420) x ABLS8447 (1-1257)

Qy	1 MetPheSerProGlyGingIleGluHsCysAlaProLeuIleGluProValIleThrCly	20
Db	1 ATGTTTCTCTCGATCAGAAATCAT-----CCATCAAGCACCGATAATATGTT	54
Qy	21 GluLeuValValLeuGlyTyrArgAlaLeuProLysGlyAspArgGlyArgGly 40	
Db	55 GAACTCTGTCGTTAGATATAATGAACTCTCCAAACGGTGATAGGAGGAA 114	
Qy	41 SerArgPheAlaLeuTyroLysArgProLysAlaArgGlyAspArgGlyArgGly 60	
Db	115 ACTAGGTTGCTTGTAAAGACTTACAGGCATAGGGCAGGGTGAGCCAGACTGTGCT 174	
Qy	61 ValIleSerThrProGlnAlaSerValAlaSerCysAlaLysGlyGlnHisSerIle 80	
Db	175 ATGCTGTGACTCCTCAGGCTSCAACGCAATTAGCAACAGACCAACGATCATACA 234	
Qy	81 TyrThrIleSerArgAsnGlnTrpValValValGluTyThrHisAspDlySerThrAsp 100	
Db	235 TATACTTTATCTGGGCCGAGCTGCTGCTGCTGATACTCATGAGCACCGAT 294	
Qy	101 MetPheGlnValAlaGlyArgSerThrGluSerProLeaPheValValThrAspThrIle 120	
Db	295 ATGTTTCAGATGGCCCGCTGACTGAAGGCCCATGTGATTGTTGTAACCTGACACGGTT 354	
Qy	121 SerGlySerGlnAsnThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheIla 140	
Db	355 CCTGGAAAGTCAGAATTCGATACAGCTGCTGAGTACAGACACTATACAGATTGCC 414	
Qy	141 CysArgIleValCysAspArgGluProTyroThraArgIlePheAlaAlaGlyPhe 160	
Db	415 TCCAGAACTCATATGTGACGGATCTCCCTTACACGACGGATTATGCTCAGGGTT 474	
Qy	161 AspSerSerIleAsnIlePheLeuGlyGluLeuAlaAlaLysTrpIleAsnProAspGly 180	
Db	475 GACTCTCAAAGAACCTTCCTGCGGAGAGCTGCCAATGGAGACATCAGATGGA 534	
Qy	181 HisMetAspGlyLeuThrThrAsnGlyValLeuValIleThsProArgGlyIlePheThr 200	
Db	535 CAGATGGATGGCTGACCAATGTTGCTGCTGATGATCCAGCAAGCTTCACA 594	
Qy	201 GluGluSerGlnProGlyValTrpArgIleSerValCysGlyAspValTyrThrIle 220	
Db	595 GAAGACCTCCAASCGCTGGATATGGAGAAGAAATATGGTGTGGGGATGTTAGCTTA 654	
RESUL	T 11	
ID	ADB48666	
XX	ADB48666 standard; cDNA; 1257 BP.	
AC	ADB48666;	
XX		
DT	09-SEP-2004 (first entry)	
XX		
DE	Human Pellino-1 encoding cDNA SEQ ID NO:3.	
XX		
KW	nuclear factor kappa B dependent transcription inhibitor;	
KW	NF-kB-dependent transcription inhibitor; Pellino-1;	
KW	P38-dependent transcription inhibitor; Pellino-1;	
KW	interleukin 1 receptor-associated kinase 4;	
KW	IL-1 receptor-associated kinase 4; antiatherosclerotic; antiarthritic; antiasthmatic; antiinflammatory; antirheumatic; antiulcer; gastrointestinal; neuroprotective; nootropic; IL-1 antagonist; IRAK protein kinase family inhibitor; NF kappa B inducing kinase inhibitor; asthma; rheumatoid arthritis; inflammatory bowel disease; Crohn's disease; ulcerative colitis; atherosclerosis; Alzheimer's disease; human; chromosome 2; gene; ss.	
KW	Homo sapiens.	
OS		
FH	Key	Location/Qualifiers
FT	CDS	1..1257 /*tag= a /product= "pellino-1"
FT		
FT		
XX	PN	W02004053092-A2.
XX	PD	24-JUN-2004.

XX PF - 09-DEC-2003; 2003WO-US039188.  
 XX PR 11-DEC-2002; 2002US-00317250.  
 XX PA (IMMUNEX CORP.  
 PA (CLEV- ) CLEVELAND CLINIC FOUND.  
 PA BIRD TA, Cozman DJ, Li X;  
 XX DR WPI; 2004-480927/45.  
 DR P-PSDB; ADP8667.  
 XX PT Identifying inhibitors of IL-1 signaling, useful for treating e.g., asthma, and rheumatoid arthritis, comprises assaying the association of a Pellino-1 polypeptide with IRAK-4 in the presence of a test compound.  
 XX PS Claim 9; SEQ ID NO 3; 81pp; English.  
 CC The present invention describes a method for identifying compounds (C) that inhibit nuclear factor kappa B (NF- $\kappa$ B) dependent transcription or p38-dependent transcription. The method comprises: (1) mixing a test compound with a Pellino-1 polypeptide; (b) assaying the association of the Pellino-1 polypeptide with IL-1 receptor-associated kinase 4 (IRAK-4) in the presence of the test compound; and (c) determining whether the test compound inhibits the association of the Pellino-1 polypeptide with a binding partner. Also described: (1) an inhibitory nucleic acid that binds to a nucleic acid encoding an amino acid sequence as described above, where the presence of the inhibitory nucleic acid within a cell inhibits the association of Pellino-1 with IRAK-4; and (2) an inhibitory polypeptide comprising an antibody fragment that binds to a polypeptide comprising an amino acid sequence as described above, where the presence of the inhibitory polypeptide within a cell inhibits the association of Pellino-1 with IRAK-4. (C) have antiartherosclerotic, antiasthmatic, antiinflammatory, antirheumatic, antiallergic, antiulcer, gastrointestinal, neuroprotective and notropic activities, and can be used as an IL-1 antagonist, IRAK protein kinase inhibitor, and NF kappa B inducing kinase inhibitor. The methods and compositions of the present invention are useful for the prevention and/or treatment of diseases or conditions associated with aberrant expression or activity of the Pellino-1 polypeptide, such as asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis and Alzheimer's disease. The present sequence encodes human Pellino-1, which is used in the exemplification of the present invention. The human Pellino-1 gene is located on chromosome 2, more specifically to 2p13.3.  
 XX SQ Sequence 1257 BP; 368 A; 264 C; 296 G; 329 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.05e-166 Length: 1257  
 Score: 19.7.00 Matches: 342  
 Percent Similarity: 90.5% Conservative: 38  
 Best Local Similarity: 81.4% Mismatches: 38  
 Query Match: 83.7% Deletions: 2  
 DB: 12.1 Gaps: 1  
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 1 ArgTrpTrpTrpCysGATCAAGAAATCAT-----COATCTAACGCCACCGTAAATATGTT 54  
 QY 21 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProAsnGlyAspArgGlyArgGargGly 40  
 55 GAACTCATTGTCTTGGATGATTAATGCTCCAAACGGTGATAGGGAGGAGGAGGAGA 114  
 DB 41 SerArgPheAlaLeuTyrIleSerGlyAsnGlyAsnGlyAspSerProSerIleVal 60  
 115 ATGAGTTGTTGCTTGTGTTAAAGACCTAGGGAATGGCTGAGCCAGCTGACTGTGCT 174  
 QY 61 ValLeuSerThrProGlnAlaSerAlaValIleSerCysLeuGlyGlnHisSerIleSer 80  
 ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:  
 DB 175 ATTCGCTTGACTCTCAGCTGCAGAACGCAATTAGCCACAAAGACCCATACATCA 234  
 QY 81 TyThrIleSerArgArgLysLysValValGluGlyIleValGluGlyIleValGlu 100  
 DB 235 TAACTTTATCTCGGCCAGACTGTGGTGAATTAATCTCATGAGCACACCGAT 294  
 QY 101 MetPheGlnValGlyArgSerIleSerProLeuLeuPheValValThrAspThrIle 120  
 PT 295 ATTTTGCGATTCGGCGCTGACTGAGGAGCCATGTTGATTCGACTGACCTGACCGTT 354  
 PR 121 SerGlySerGlnAlaSerThrAspGluAlaGlnIleThrSerIleSerArgPheAla 140  
 DB 355 CCTCGAACCTCAAGTAATCTGTGATACACAGTCGAGTCAGACTATCACAGATTC 414  
 QY 141 CysArgIleValCysArgArgLysIleProGluProTyroValAlaArgPheAlaLysPhe 160  
 CC 415 TCGAGAACATATGTCAGGAGATCCCTTACAGCACGATTTGCTGAGCTGAGGTT 474  
 QY 161 AspSerSerIleAsnIlePheLeuGlyGluIleValAlaLysIleProIleAsnIlePhe 180  
 CC 475 GACTCTCAAAACACCTCTCTGGGAGAGCTCCAAATGGAGACATCAGATGA 534  
 QY 181 HisMetArgPheIleUthThrIleGlyValGluValMetHisProArgGlyGlyPhe 200  
 CC 535 CAGATGAGGCTTGACCACTATGGTCTCTGAGCTACACCCATCACCGATGGTCA 594  
 CC 201 GluGluGluGlnProGlyValTrpArgGluIleSerValCysGlyAspValTyroIle 220  
 CC 655 CGTGAACAGATGGCTCAGCAGAAATCGCTGTTGGAATGTTGAGCTGAGCTGAGCA 714  
 CC 595 GAGACTCTCAACGCTGAAATGAGCTTACAGCACGATTTGCTGAGGAATGTTAGCTTA 654  
 QY 241 GluAspGlySerLeuIleAspLeuCysGlyIleThrIleLeuTrpGlnThrAlaAspGly 260  
 CC 715 CAAGATGCTGCTGTAATGACCCTGCTGAGCTGACTGCTGAGG 774  
 CC 251 LeuPheIleIleProTrpGlyIleAspIleGluIleLeuAspGlyGluIleLeu 280  
 CC 775 CTTCGCCACACTCTTACGCTGAGCAATGAAATGTTGAACTGACCATCTGACA 834  
 DB 281 ArgProGlnGlyAspValGlyIleAsnIleValAspProSerIleAsnArgIleGlu 300  
 QY 835 CGACCTCGTGCCCTGAGGGTCACACACTGACATTCCTAGTAAAGGAGAAC 894  
 DB 301 ValValGluGluGlyGlnProTrpIleAspSerCysGlyHisValHisGlyTyrHis 320  
 DB 895 GTTGATGAGAAACACCATCGGGTAAATCTAACCTGGCCATGTCATGCTCAT 954  
 QY 321 AsnTrpGlyIleArgSerAspThrGluIleAsnGluArgGluGlyAspMetCysArgThr 340  
 DB 955 AACGGGCAACAAAGAAAGAAAGCTGCTGCAAGATGTTGAAATGTCCTPATGTTGACTCT 1014  
 QY 341 ValGlyProTrpValProLeuIlePheLeuIleCysGluAlaLysPheTyrValAspAlaGly 360  
 DB 1015 GTTGGCCCTATGTTCTCTCTGCTGCTCTGATGAGCTGGATTTGTTGAGGCGCC 1074  
 QY 351 ProProThrHisAlaPheIleProCysGlyHisIvaCysSerGlyAspSerAlaLysTyr 380  
 DB 1075 CCCTCAACCCATCGGTTAGCCCGTGGGCGTGTGTTGAGAAAGACAATGCGCTAT 1134  
 QY 381 TrpSerGlnIleProLeuProIleGlyThrIleAlaPheIleAlaAlaCysProProCys 400  
 DB 1135 TGTCCCGATCCACTTCTCTCATGGTACTCTACTTTCAGGAGCCCTGCTTGT 1194  
 QY 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleLeuIlePheGlnGlyProLeuAsp 420  
 DB 1195 GCACATCGTGTCTGCTGAGCTACATGACTTCACTGAGGACCTGCTAGAC 1254  
 RESULT 12  
 ID ABX05095 standard; cDNA; 1304 BP.







Db 1362 ACTGGGGAAACMAAGAAGAACCTGATGAAAGATCCTGAATGTCATGTGAGTCT 1421  
 Qy 341 ValGlyProTyValProLeuPheLeuGlyGluGlySerGluAlaGlyPheTyValAlaPheGly 360  
 Db 1422 GTGTTGCCTATGTCCTCTGTTGAGCTGAGCTGGATGTTAGTGCGCC 1481  
 Qy 361 ProProThrHisAlaPheThrProCysGlyHisValCysSerGluLysSerAlaLysTyr 380  
 Db 1482 CTGCCACCAAGCTGGCTTAGCTGCGCTGGGCTGTTGCTGAAAGAACACTGCTAT 1541  
 Qy 381 TrpSerGlnIleProLeuProHisGlyThrHisAlaPheHisAlaAlaCysProHeCys 400  
 Db 1542 TGTCCAGATCCACTCTCTGAGCTACTCATCTACTTCACTTCAGTCAGCTGTCCTTGT 1601  
 Qy 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleLysLeuIlePheGlnGlyProLeuAsp 420  
 Db 1602 GACATCAGTGTCTGAGAACAGGTCTACATCAGTCAGCTTCAAGGACTCTAGAC 1661  
 RESULT 15  
 ADP83102  
 ID ADP83102 standard; cDNA; 7136 BP.  
 XX  
 AC ADP83102;  
 YX  
 DT 26-FEB-2004 (first entry)  
 XX Human Pellino homologue 1 gene, overexpressed in cancer.  
 XX Human; Pellino homologue 1; Pellino1; cancer; cytostatic; vaccine;  
 KW gene therapy; gene; oncogene; bb.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 PT CDS /\*tag- a  
 PT WO2003100000-A2.  
 PN 04-DEC-2003.  
 PR 22-MAY-2003; 2003WO-US016049.  
 PR 24-MAY-2002; 2002US-038266P.  
 PR 25-JUL-2002; 2002US-0398099P.  
 DR (TULLA-) TULARIK INC.  
 XX Li, J., Mu D., Yang J.;  
 XX WPI; 2004-035118/03.  
 DR P-PSDB; ADP83103.  
 DR GREN BANK, NM\_020651.  
 PT Diagnosing a cancer in a mammal comprises determining RacQ5, CTXL,  
 PT USP13, MCL1, or Pellino 1 gene copy number in a biological sample from a  
 PT region of the mammal that is suspected to be precancerous or cancerous.  
 PS Claim 179; SEQ ID NO 9; 174pp; English.  
 XX  
 CC The present sequence is that of the gene encoding human Pellino homologue  
 CC 1 (Pellino), a protein associated with the kinase domain of activated  
 CC Pelle. The invention is based on the finding of the overexpression of  
 CC Pellino and other genes (RacQ5, CTXL, USP13 and MCL1) in certain  
 CC cancers, including breast cancer, colon cancer, lung cancer and ovarian  
 CC cancer, and the frequent amplification of these genes in cancer cells.  
 CC The genes, and their expression products, can be used diagnostically or  
 CC as targets for cancer therapy. They can also be used to identify and  
 CC design compounds useful in the diagnosis, prevention and therapy of  
 CC tumours and cancers, in vaccine development, and in methods for  
 CC determining the efficacy of a treatment regime. A claimed method for  
 CC inhibiting cancer or precancerous growth, especially in ovarian or lung  
 CC tissue, uses an inhibitor that interacts with Pellino DNA or RNA. The

CC inhibitor is a small interfering RNA (siRNA), microRNA (miRNA), an antisense RNA, and antisense DNA, a decoy molecule, a decoy DNA, a ribozyme or small molecule.

Sequence 7136 BP; 1545 A; 1333 C; 1399 G; 2459 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	9.67e-165	Length:	7136
Score:	1917.00	Mat. Chas:	342
Percent Similarity:	90.5%	Conservative:	38
Best Local Similarity:	81.4%	Mismatches:	38
Query Match:	83.7%	Indels:	2
DB:	12	Gaps:	1

us-10-041-030-4 (1-420) x ADP83102 (1-7136)

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 Qy 21 GluLeuValValLeuGlyTyrglyYalaleuProArgLysAspArgYVargArgLys 40  
 Db 4093 GIACTCATGTCCTAGCTATAATGGCTCTCCCAAATSGCGATGAGGAGGAGAA 4152  
 Qy 41 SerArgPheAlaLeuTyrylSargProLysAlaAsnGlyVallysProSerThrValHis 60  
 Db 4213 ATGGCTTGTACTCTCAGTCAGCTGCTGAGCAAGGCCATGGTCAAGCCAGCACTGCT 4212  
 Qy 61 ValLeuSerThrProGlnAlaSerLysValAlaSerCysLysGlyClnHsSerIle 80  
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 Qy 81 TyrThrIleSerArgGangInThrValValValGlyTyrrHsIlePheAspThrAsp 100  
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 Qy 101 MetPheGlnValGlyArgSerThrGluSerProLeAspPheValValThrAspThrIle 120  
 Db 4333 ATGTTTCAGATGGCCGGTGCAGTCAGAAAGCCCATGGTCAAGCCAGCTTGTACTACAGGTT 4392  
 Qy 121 SerGlySerGlnAspThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140  
 Db 4393 CCTGGAACTGAGTAAATCTGATACACAGTCAGTCAGTACAAAGCTATGATGATTGCG 4452  
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 Db 4453 TCCAGATCATAGTCAGTCAGGATACCTCCCTTACAGCAAGGATTATGCTGCAGATT 4512  
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 Qy 201 GluGluSerGlnProGlyValTrpArgGluLeSerValCysGlyAspValTyrrIle 220  
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 Db 4693 CGTGAACACAGATCGGCCTAGCAGAGGAGAAATGGGAAATTGAAACCATCTGTA 4752  
 Qy 241 GluAspGlySerLeuLeuAspLeuCysGlyAlaThrLeuLeuThrArgThrAlaAspGly 260  
 Db 4753 CAGATGGCTCTTAATGACCTCTGGCAACATGTTATGGCTGAGTCAGTCAGGAGGC 4812  
 Qy 261 LeuPheHisIleProThrGlyLysBisIleGluLeuIleArgGlnGluLeuAsnAla 280  
 Db 4813 CTTCCACACTCTGAGCTGAGCTTAACTGAGCAATGAACTCAATGCA 4872  
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Qy	3.41	ValGlyProTrpValProLeuTrpLeuGlyCysGluAlaGlyPheTrpValAlaGly	360
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Qy	3.81	TrpSerGlnIleProLeuProHisGlyThrHisAlaPheAlaAlaLysProPheCys	400
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Search completed: March 2, 2006, 05:14:48  
Job time : 823 secs



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Score:	2290.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
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Matches:	420
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Mismatches:	0
Indels:	0
Gaps:	0
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Db	51 ATGTTTTCCTCCGCCAGAGAACCTGGCCCAATAGGCGCAGTGAAATACGG 110
QY	21 GluLeuValValLeuGlyTyrArgAlaLeuProArgLysAspArgGlyValArgLys 40
Db	111 GAGCTGGAGCTGCTGCTGCTACATGCTGCTTACCCATGGAGTAGAGGACGGAGAA 170
QY	41 SerArgHealaLeutValLeuGlyProValAlaAlaGlyValValProSerValVal 60
Db	171 ACTAGATTGGCTCTACAGGCCAGGCAATGCTGAAACAGACGGCTCAT 230
QY	61 ValIleSerThrProGlnAlaSerLysAlaIleSerCysLysGlyGlnIleSerIleSer 80
Db	231 GTGATTCACGCCAGGCTACAGCTTACGCTGAAAGCTCACACATATCC 290
QY	81 TyrThrLeuSerArgAspGlnLysValValGluTyrThrHisAspLysAspThrAsp 100
Db	291 TACACTTGTCAAGAACTGAGCTGTGGTGGTGGAGTACACATGATAAGGATCGAT 350
QY	101 MetPheGlnValGlyArgSerThrGlnSerProIleLeuPheValValThrAspThrIle 120
Db	351 ATGTTTCAAGGCTGGAGCTACAGAAAGCCATATGCTCTTGCTGAGACGATT 410
QY	121 SerGlySerGlnAsnThrAspGluAlaGlnIleThrGlnInserThrIleSerArgPheIa 140
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QY	161 AspSerCysLysIleIlePheLeuGlyGluValAlaAlaLysIlePheAsnProAspGly 180
Db	531 GACTCTTCACAAACCATATTCTGTGAGAAAGCGAACCCCGACGCC 590
QY	181 HisMetIleAspGlyIleIleThrAspGlyValLeuValLeuValMetIleAspArgGlyGlyPheThr 200
Db	591 CACATGGATGGCTCACTACTAAATGGCCTCTGGATGATCCAGAGGGGGCTTCACC 650
QY	221 ArgGluIleThrArgSerAlaGlnGlnArgGlyIleLeuValGluSerGluThrAsnValLeu 240
Db	651 GAGGAGTCCAGGCCGGGGCTGGCGGAGATCTCTGTGAGAGCTGACCTTG 710
QY	241 GluAspGlySerIleIleLeuLeuIlePheIleCysGlyIleAlaThrLeuLeuIlePheGly 260
RESULT 2	
LOCUS	BC009476
DEFINITION	Homo sapiens pellino homolog 2 (Drosophila), mRNA (cDNA clone MGC:15066 IMAGE:3942712), complete cds.
ACCESSION	BC009476
VERSION	BC009476.2 GI:33872093
KEYWORDS	MGC
SOURCE	Homo sapiens (human)
ORGANISM	Homo Sapiens
REFERENCE	1. (bases 1 to 1811) Strauberg RL, Feingold EA, Grouse LH, Derge JC, Klausner RD, Collins FS, Wagner L, Shevchenko CM, Schulz GE, Altshuler DP, Zeeberg B, Butow KH, Schaeffer CF, Bhat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Cabarrot TL, Scheetz TE, Brownstein MJ, Uddin TB, Tobiishi K, Carninci P, Prange C, Raha SS, Loqueland NJ, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McElwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay JW, Bulyk SW, Villalon DK, Muzny DM, Sodergren EJ, Iu X, Gibbs RA, Fahey J, Helton E, Kettman M, Madan A, Rodriguez S, Sanchez A, Whiting M, Madan A, Young AC, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smialowski DE, Schnerch A, Schein JE, Jones SJ and Marra MA.
AUTHORS	Mammalian Gene Collection Program Team
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLMED	12477332
REFERENCE	2 (bases 1 to 1811)
AUTHORS	Director MGC Project.
TITLE	Direct Submission
JOURNAL	Submitted (25-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
QY	261 LeuPheIleSerProThrGlnIleAspIleLeuArgGluGlnIleLeuAlaIala 280
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QY	281 ArgProGlyCysProValGlyLeuAlaThrLeuAlaProSerIleAspArgLysGlu 300
Db	891 GGCCTCACTGTCCTGTCGGAGCTGCAACCCGCTCCACCATCAAGGAGAG 950
QY	301 ValValGluGluIleValProAlaValValLeuSerCysGlyIleValHisGlyThr 320
Db	951 GTGGTGGAGGAAGACAGCAGCCCTGGCATATCTGAGTGTGCGCACTGCGACGGTACAC 1010
QY	321 AsnTrpGlyIleValArgSerIlePheIleAspGluValCysProMetCysArgThr 340
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Db	1071 GTGGGCCCCATATGTCCTCTGCTGCTGAGTTATGTAAGGCGAGGA 1130
QY	361 ProProThrlSAlaPheThrProCysGlyIleValCysSerGlyUssSerAlaLysThr 380
Db	1131 CGCGCAACTCTGCTTCTACTCCCTGTGCTGACTCTGCTGCTGCAAATAC 1190
QY	381 TrpSerGlnIleProLeuProIleGlyIleValAlaPhenylalanineAlaLeuCysProProheCys 400
Db	1191 TGGCTCAGTCCGCTGCTCATGACTCTATGCTTACCGCTGCTGCTGCCCTCTGT 1250
QY	401 AlaThrGlnIleValGlyIleGluGlnIleValCysIleLeuIleLeuIlePheGlyProIleAsp 420
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QY	2771 CAGGAGGCTCCCTCATGGCTGCTGAGGACTCTCCCTGGAGAAAGCAGCAGATG 830

Page 3

**REMARK**  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
On Aug 19, 2003 this sequence version replaced gi:14550456.  
**COMMENT**  
Contact: MGC help desk  
Email: [cdaps@remail.nih.gov](mailto:cdaps@remail.nih.gov)  
Tissue Procurement: DCRB/DRP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)  
DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbiology.org>  
contact: amadan@systemsbiology.org  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kerteman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

**FEATURES**

source	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: <a href="http://image.liln.gov">http://image.liln.gov</a>
	Series: IRL Plate: 25 Row: 9 Column: 3
	This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10864062.
	Location/Qualifiers
1.	.1811 /organism="Homo sapiens" /mol_type="mRNA" /db_xref=taxon:9606" (clone=MGC:1506 IMAGE:3942712" /tissue type="lung, small cell carcinoma" /clone Lib="NIH MGC_7" /lab host="DH10B-R" /note="Vector: pOTB7" 1. .1811 /genes="PELI2" /ab_xref=GeneID:57161" 287. .1549 /genes="PELI2" /codon_start=1 /product="pellino 2" /protein_id="AAH09476.1" /db_xref=GI:14550457" /db_xref=GeneID:57161" /translation="MFSQPCBECPKPKVKGCBLVVGYNGALPNGRGRKSRSFA LYKRPKANGVKPSITVWVPOASIAISCKGHSYTSRSNOTVWVETHDKDTPDMF OVRGRTESPIDPVWDTIQQSNTDQAQTOSTISRPARIVCORNEPPTARFAAGF DSSKNIFLGEKAQAKWVNPDGMDGATLWVWRGGTTEESPGVMEKISVGDVY TLETRRTSAQDQGLVUNLAFPSINRKEVEKOPWAVLSCGNGVHGRHSDTBANER INAAPQCQGINTLAFPSINRKEVEKOPWAVLSCGNGVHGRHSDTBANER CPMCRKIVGPPVPLWIGCEAQPYVDAQPPHTAFTPGCHVSEKSAKXWSOPLPHGTA FHACCPFCATQLOVQSGNCIKLIFPQDID"
ORIGIN	Alignment Scores: pred. No.: 1.73e-166 Length: 1811 Score: 2390.00 Matches: 420 Percent Similarity: 100.0% Conservative: 0 Best Local Similarity: 100.0% Mismatches: 0 Query Match: 100.0% Indels: 0 DB: 8 Gaps: 0
US-10-041-030-4 (1-420) x BC009476 (1-1811)	

**QY**  
1 MetPheSerProGlyGlnGluGluLysCysAlaProAsnLysGluProValLysTrpGly 20  
Db 287 ATGTTTCCCTCGCCAGGAGAACCTGCGCCCATAGGAGCAGGAAATCGGG 346  
Db -347 GAGCTGGTGGTCGGTCACTGCTGCTTACCCATGGATGAGGAGGGAGGA 406  
41 SerArgPheAlaLeuTyrLysArgProLysAlaAsnLysValLysProSerThrValHis 60  
Db 407 AGTAGATTGGCCCTCTACAGCGGCCAGGCAATGGTGCAACCCAGCGCCAT 466  
61 ValLeuSerThrProGlnAlaSerLysLysAlaSerCysLysGlyGlnHisSerIleSer 80

Db	467	GCGATTCACGCCCGCCGCTCCAGCTTCAAGCTTCAGTCGAGGCAACGTATTC
Qy	81	Tyr-ThreuserArgCysAlaLysValValValgluThrIleAspAspPheAsp
Db	527	TACCTTGTCAGGAACTCAGACTGTTGGTGGTGAACATCATATAAGGATAGGAT
Qy	101	Met-PheGlnValGlyArgSerThrLysSerProIleAspPheValValThrIle
Db	587	AAGTTGAGGAGGAGATCACAGAACTGTTGGTGGTGAACATCATATAAGGATAGGAT
Qy	121	SerGlySerGluAlaThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla
Db	647	TCTGGCACCAGAACGAGCAGCCAGTCACTGACTTGGTGTGTTGACAGATT
Qy	141	CysArgIleValCysAspArgAspGluProThrAlaArgIlePheAlaLysPhe
Db	707	TGAGGAGTGGTGGCAGACAGGATGACCTTACAGCAGCGATATTCGCGCCGATT
Qy	161	AsnSerSerLeuAsnIlePheAlaGlyGluValAlaLysIleAspAspGly
Db	767	GACTTCTCAAAACATTAATTGTTGAGAAGAGGCGCAAGTACGACCACTATCCAGGTTGCC
Qy	181	HisMetAspGlyLeuThrThrAspGlyValLeuValMetHisProArgGlyGlyPhe
Db	827	CAATGGATGACTCTACTATGAGGCTTGGATGATCCTCTGGAGGCTTAC
Qy	201	GlugluSerGlnProGlyValTrpArgGluLeuSerValCysGlyAspValTyrrIle
Db	887	GAGGAGTGGCACCACCGGCGACGCTGCGCGAGATCTCTCTCTGAGGATGTTACACTG
Qy	221	AspGluThrAspSerAlaGlnGluArgGlyValAspLeuValIgUserGluThrAsnIleu
Db	947	CGAGAACCCAGCTGGCCGACGACGAGGAGCTGGTGGAAAGGAGACCTG
Qy	241	GlnAspGlySerLeuIleAspLeuCysGlyAlaThrIleLeuTrpArgThrAlaAspGly
Db	1007	CAAGGAACTCTCTATGACCTGTTGGGACACTCTCTGGAGAAGCAGGG 1066
Qy	261	LeuPheIleSth-ProThrGlyLysIleGluAlaLeuArgGlnGluIleAsnAlaAla
Db	1057	CTTTCTACTCCACTCAGACCATAGAGCCCTCCGGAGGATTAACCGGCC
Qy	281	AspProGlnCysProValGlyLeuAlaThrIleAlaPheProSerIleAspArgYsGlu
Db	1127	CGCCCTCTGTCGTCCTGGGCTCACACCTGGCCCTCCACGCTCACAGGAGAG
Qy	301	ValValGluGluLysGlnProProAlaTyrLeuSerCysGlyIleValHisGlyThrIle
Db	1187	GRCGGGGGGAGAGCAGCCCTGGGATATCAGTGTGGCCACTCTGCACGGGAAACAC
Qy	321	AspTrpGlyIleSargSerAspThrGluAlaBngIleArgGluCysProMetCysArgThr
Db	1247	AACTGGGCCCCCTGGAGTAGCACTGGGGCAACGAGGAGGTGCCCCTGGAGACT
Qy	341	ValGlyProTrpValProLeuIlePheGlyCysGluAlaGlyPheYrValAspAlaGly
Db	1307	GTCGGGCCCTATGTCGCTCTGGCTGCGCTGGTGGAGGATTTATGTRAGCCAGGA
Qy	361	ProProThrIleAlaPheThrProCysGlyIleValCysSerGluLysSerAlaLysTyr
Db	1367	CCGCCAACTCAGTCCTTCACCTCTCTGGAGACGTTGCTGGAGAGTCGCAAAATAC
Qy	381	TrpSerGlnIleProLeuProIleGlyYThrIleAlaPheHisAlaAlaCysProPheCys
Db	1427	TGGTCGATCCGGTGGCTCATGAACTCATGCTTCACTGCTTCCTCTG
Qy	401	AlaThrGlnLeuValGlyGluGlnIleCysIleLeuIlePheGlyProIleAsp
Db	1487	GTCTACAGCTGGTGGGAGCAAACTGTCATCAAAITATTTCCAAGGTCCTAAATGAC

LOCUS	BD190328	5579 bp	DNA	linear	PAT 17-JUL-2003	Qy
DEFINITION	Etk1 phosphorylation related gene.					
ACCESSION	BD190328					
VERSION	BD190328.1					
KEYWORDS	W0 03008589-A/68;					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
Bukar-Yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.						
REFERENCE	1 (bases 1 to 5579)					
AUTHORS	Matsuaki, O., Matsuda, A., Nagano, Y. and Suzuki, N.					
TITLE	Etk1 phosphorylation related gene					
JOURNAL	PATENT: WO 03008589-A 68 30-JAN-2003; ASAHI KASEI CORP,OSAMU MATSUZAKI,AKIO MATSUDA,YUKIKO NAGANO, NAOMI SUZUKI					
COMMENT	OS	Homo sapiens (human)				
	PN	WO 03008589-A/68				
	PD	30-JAN-2003				
	PF	15-JUL-2002	WO 2002JP007174			
	PR	18-JUL-2001	JP 01P 218204, 31-AUG-2001	JP 01P 263450	PR	
	21-JAN-2002	JP 02P 012176				
	PI	OSAMU MATSUZAKI AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI PC CI2N15/54, CI2N9/11, G01N33/05, G01N33/15, C07K16/40, A61K39/385, PC A61K31/711				
	CC	Etk1 phosphorylation related gene				
	FH	Key	Location/Qualifiers			
	FT	CDS	Location/Qualifiers	(177) . (1436).		
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ORIGIN						
Alignment Scores:						
Pred. No.:	6.29E-166	Length:	5579			
Score:	2290.00	Matches:	420			
Percent Similarity:	100.0%	Conservative:	0			
Best Local Similarity:	100.0%	Mismatches:	0			
Query Match:	100.0%	Indels:	0			
DB:	6	Gaps:	0			
US-10-041-030-4 (1-420) x BD190328 (1-5579)						
Qy	1	MetPheSerProGlyGlnGluLysAlaProAsnLysGluProValTyrGly	20			
Db	177	ATGTTTCCTGGCAGGAGACTGGCCCCCAATAGGCCAGTGAATACGGG	236			
Qy	21	GlutLeuValValLeuGlyTyrAspAlaLeuProAsnGlyAspArgGlyTargArgLys 40				
Db	237	GAGCTTGTGAGTCGCTGGTACAATGCTGCTTACCAATGGAGAAGGGAA	296			
Qy	41	SerArgPheAlaLysThrLysArgProValAlaLysGlyValLeuProSerThrValHis 60				
Db	297	AGTAGATTGGCCCTCTACAGGCCAACGCGAACATGGCTCACACCACCGTCCAT	356			
Qy	61	ValLeuSerThrProGlnAlaSerLysAlaLeuSerCysLysGlyGlnLysSerLeu 80				
Db	357	GTGATATGCCGCCAGGCCAGGATCCAGCTGCAAGGTCACCACTGATATCC	416			
Qy	81	TyrThrLeuSerArgArgInthrValValGluTyrThrHisAspLysAspThrAsp 100				
Db	417	TACACTTGTCAGGAACTGAGCTGCTGGTGGTACACATGATAAGGATAGGAT	476			
Qy	101	MetPheGlnValGlyArgSerThrGluSerProIleAspPheValValThrPheIle 120				
Db	477	ATGTTCACTGGGAGACAGGACGACGCCAGCATGAGCACTGAGTCGGTGC	536			
Qy	121	SerglySerGlnAsnThrAspGluAlaGlnIleThrGluSerThrIleSerArgPheAla 140				
Db	537	TCTGGCAGGCCAGAACGCGACGCCAGCATGAGCACTGAGTCGGTGC	596			
RESULT	4					
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LOCUS	AF302502	5579 bp	mRNA	linear	PRI 05-JUL-2001	
DEFINITION	Homo sapiens pellino 2 (PEL12) mRNA, complete cds.					
ACCESSION	AF302502					
VERSION	AF302502.1					
KEYWORDS	.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
Bukar-Yota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.						
REFERENCE	1 (bases 1 to 5579)					
AUTHORS	Reich, K., Jockusch, H. and Schmitt-John, T.					
TITLE	Assignment of homologous genes, Pelli1/PEL12 and Pelli2/PEL12, for the Pelle adaptor protein Pelliino to mouse chromosomes 11 and 14,					



source	1. .5921	QY	221 ArgGluThrArgSerLysLysGlnArgGlyLysLeuValGluSerCleuThrAsnValLeu 240	
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		DSSNIFIGEKAQKWKNPQHMDGUTTGVLMPRGTEBEPQGVREISQGDV 1221		
		TURTRSAQORGKLVESETVNLDGSLSDLCATWLRADGHPTKHTALRQE 1221		
		CPIKORTPGVGLNTLAFPSRINRKEVNEBQPLWCGTIVHGRCRSDTANERB 1221		
		PHACPPCATOLVGEQNCLIKIQRQPD" 1221		
501. .1763	Environment Scores:			
501. .1763	Seq. No.:	6.72e-166	Length:	5921
501. .1763	Score:	2290.00	Matches:	420
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501. .1763	Local Similarity:	100.0%	Mismatches:	0
501. .1763	Identity:	0	Indels:	0
501. .1763	Gaps:	6		
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501. .1763	501 ATGTTTCCTGGCCAGGAGGAACTGCGCCCCATAGAGGCCAGTGAAATCGGG 560	Db	1281 CTTTTCTACTCCAACTCAGAACATAGAGGCCCTGGCCAGAGATAACGCC 1340	
501. .1763	21 GlutLeuValLeuLysTyrAsnGlyAlaLeuProAsnGlyAspArgGlyArgGly 40	QY	281 ArgProGlnCysProValGlyLysAsnThrLeuAlaPheProSerAlaLeuArgGly 300	
501. .1763	561 GAGCTGTGGAATCTGGATCACATGGCTTACCCATGGAGATGAGGAGGAGAA 620	Db	1341 CGGCCCTCAGTCCTCTGGCTCACACCTGSCCTCCASCTCACAGGAAAG 1400	
501. .1763	41 SerArgPheAlaLeuTyrLysArgProLysAlaAsnGlyLysProSerThrValHis 60	QY	301 ValValGluGluLysGlnProProAlaLysLeuSerCysGlyLysValHisGlyTyrHis 320	
501. .1763	61 ValLeuSerThrProGlnAlaSerLysAlaSerCysLysArgLysValHisSerIleSer 80	Db	1401 GTGGGAGGAGGAGGAGGCCGATCTCTGAGCCACCTGTCGGCACTGGGACGGGACAC 1460	
501. .1763	621 AGTAGATTTCCTCTACAGACGGCCAAAGCTTGTGTCACACCGCCAT 680	QY	321 AsnTrpGlyLysAspSerAspThrGluLysAsnGluLysGluCysProMetCysArgThr 340	
501. .1763	681 GTGATTTCCACCCCCAGGATCCAGGCTATCAGTGCAAGGTCACAGTATTC 740	Db	1461 AACTGCGGCCATCAGGGATGACACGGGGGCCACAGGAGGTGTCCTAGTGAGGACT 1520	
501. .1763	81 TyrThrLeuSerArgGlnGlnThrValValAlaGluLysTyrThrHisAspLysAspThrAsp 100	QY	341 ValGlyProTyroValProLysTyrLysGluAlaGlyProTyrValAspAlaGly 360	
501. .1763	741 TACACTTGTCAGGATCAGTCACTGCTGCTGGTGGAGGATCAGCATCAAGATGGAT 800	Db	1521 GTGGGSCCTCTGTCCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1580	
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	LOCUS	AR483568		
	DEFINITION	Sequence 7 from patent US 6703487.	1263 bp	
	ACCESSION	AR483568	DNA	
	VERSION	AR483568.1	linear	
	KEYWORDS	GI:47246652	PAT 14-MAY-2004	
	SOURCE			
	ORGANISM	Unknown.		
	REFERENCE	Unclassified.		
	1. (bases 1 to 1263)			
	AUTHORS	Bird, T.A. and Cosman, D.J.		
	TITLE	Human pellino polypeptides		
	JOURNAL	Patent: US 6703487-A 7 09-MAR-2004;		
		ImmuneX Corporation; Seattle, WA;		
	FEATURES	WOX; Location/Qualifiers		
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	Best Local Similarity:	99.8%	Mismatches:	1
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US-10-041-030-4 (1-420) x AR483568 (1-1263)				



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Db	481 GACTCTCCAAACATTTCTTGAGTAAGCAGCAAGTGAACCCGAGCC	540
Oy	181 HisMetAspGlyLeuThrThrAspGlyValLeuValMetHisProArgGlyGlyPheThr	200
Db	541 CACATGGATGGGCTACTAATGGCCPCTCTGTCGATCCACGGGGCTTCACC	600
Oy	201 GluGluSerGlnProGlyValLeuValArgGluLeuSerValCysAspValTyrThrIeu	220
Db	601 GAGAGATCCAGCCGGGCTCGCGCGATCTCTGCTGAGATGTCACCTTG	660
Oy	221 ArgGluLysArgSerAlaLeuGlyValLeuValGluSerGluLysValLeu	240
Db	651 CGAGAACGAGGTCGGCCAGCACGAGCTGGAGCTCCACAGGAGCTTCACC	720
Oy	241 GluAspGlySerLeuLeuAspLeuCysGlyAlaThrLeuLeuTrpGlyThrAlaAspGly	260
Db	721 CAGGAGCCTCCCATGACTGACTGCTGGGCACTCTCTCTGAGAACAGCTGG	780
Oy	261 LeuPheIleThrProThrGlyValLeuValAspGlyLeuValLeuValLeu	280
Db	781 CTTTCTGACTCAACTCAGAACACATAGAACCCCTCGCAGGAGTTAACGCC	840
Oy	281 ArgProGlnCysProValGlyLeuAspLeuAspLeuAspLeuAspLeuAspGlyGlu	300
Db	841 CGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
Oy	301 ValValGluGluLysGlnProTrpAlaLeuSerCysGlyAlaValHisGlyTyrHis	320
Db	901 GTGCTGGAGGAGAACGACCCCTGGCATCTAGTCTGGCACGTCACGGTACCC	960
Oy	321 AsnTrpGlyHisAlaArgSerAspThrGluAlaAsnGluGlyGluCysProMetCysArgThr	340
Db	961 AACGGGCCATCGAGTCACGGGCAACAGGAGCCAAAGAGGAGTCCTGAGACT	1020
Oy	341 ValGlyProTrpValProLeuTrpLeuGlyGlyGluValGlyLeuValAspAlaGly	360
Db	1021 GTGGGCCCTATGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080
Oy	361 ProProThrHisAlaPheThrProCysGlyAlaValCysSerGluLysSerAlaLeuTyr	380
Db	1081 CCGCCAACCTCATCTTCTACTCCCTGCTGCTGCTGCTGCTGAAATAC	1140
Oy	381 TrpSerGlnIleProLeuProHisGlyThrHisAlaPheHisAlaAlaCysProHeCys	400
Db	1141 TGGCTCTGAGATCCGTTGCTCTCATGACTCTCATTCACCTGCTGCCCTTCGT	1200
Oy	401 AspThrGlyLeuValGlyGluGlnAspCysIleValLeuPheGlyGlyProIleAsp	420
Db	1201 GCTACACAGCTGGTGGGAGCAAACTCTCATCAATTATTTCGAGTCATTCATGAC	1260
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LOCUS	AR483567	Sequence 5 from patent US 6703487.
DEFINITION	Accession AR483567.1	GI:47246651
ACCESSION	AR483567.1	GI:47246651
KEYWORDS	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 1260)	
AUTHORS	Bird, T.A. and Cosman, D.J.	
TITLE	Human Peptide Polypeptides	
JOURNAL	Patent: US 6703487-A 5-09-MAR-2004;	
Immunoxx Corporation; Seattle, WA;		
WOX;	Location/Qualifiers	
FEATURES	Source	1. .1260

QY 301 ValValGluGluLysGlnProTrpAlaTyrLeuSerCysGlyHisValHisGlyTyrHis 320  
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QY 321 AsnTrpGlyHisArgSerAspThrPheValAlaAngIuargGluCysProMetCysBArgThr 340  
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Db 1018 GGGGCCCTAGTCCTCTGGCTGTGGCTGAGGAGATTATGTCATGGGA 1077  
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LOCUS AX298077 1260 bp DNA linear PAT 26-NOV-2001  
DEFINITION Sequence 5 from Patent WO0183739.  
ACCESSION AX298077.1 GI:17128159  
VERSION 1  
KEYWORDS Mus musculus (house mouse)  
ORGANISM Mus musculus; Buteraria; Euarchonta; Chordata; Craniata; Vertebrata; Euteleostomi;  
REFERENCE 1  
AUTHORS Bird, T.A. and Cosman, D.J.  
TITLE Human pellino polypeptides  
JOURNAL Patent: WO 0183739-A 5 08-NOV-2001;  
IMMUNEX CORPORATION (USA)  
FEATURES source  
ORIGIN  
Alignment Scores:  
Pred. No.: 7.21e-158 Length: 1260  
Score: 21.75.50 Matches: 399  
Percent Similarity: 97.4% Conservative: 10  
Best Local Similarity: 95.0% Mismatches: 10  
Query Match: 6 Indels: 1  
DB: Gaps: 1  
US-10-041-030-4 (1-420) x AX298077 (1-1260)  
QY 1 MetPhaserProgIgGnGluLysGlnAlaProAlaLysGluProValIuasTyrGly 20  
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QY 21 GluLeuValValLeuGlyTyrAsnGlyAlaLeuProLeuGlyAspArgGlyArgArgGly 40  
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QY 101 MetPheGlnValGlyArgSerThrGluProLeuAspPheValValThrAspThr 120  
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QY 121 SerGlySerGlnAsnThrAspGluLysIleLeuPheGlyPheLeuProLeuCys 400  
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QY 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleIleLeuPheGlyPheLeuProLeuCys 420  
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QY 181 HisMetAspGlyLeuThrIleAspGlyValLeuValMetHisProArgGlyGlyPhe 200  
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QY 201 GluGluSerGlnProLyValTrpArgGluLeuSerValCysGlyAspValTyrIle 220  
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QY 221 ArgGluLhrArgSerAlaGlnGlnArgGlyIleLeuValGluSerGlnThrAsp 240  
Db 658 CGAGAGCAGCTGCCCCAGGAAAGGAAAGCCAAATGAAAACCTGATGGA 717  
QY 241 GlnAspGlySerLeuIleAspIleCysGlyIleAlaLysIleLeuPheGly 260  
Db 718 CGAGACGGCTCTCTGTTGACCTGTCGGAGACCCACTCTCTGGAGATTCACCTG 777  
QY 261 LeuPheHistidProTrpGlyLysIleIleLeuIleLeuIleAspAla 280  
Db 778 CTTTTCAGCTGCTACTCTAGAGACATACAGCCCTCCGGAGAGATCATGAGCC 837  
QY 281 ArgProGlnCysProValGlyLeuAsnThrIleLeuPheProSerIleAspArgThrAla 300  
Db 838 CGACCCAGTCGCCCCCTGGCCCTAACCCCTGGCTTCCAGCTAACGGGAGAA 897  
QY 301 ValValGluGluLysGlnProTrpAlaTyrLeuSerCysGlyHisValHisGly 320  
Db 898 GCGTGGAAAGAAGCAGCCCTGGGCTACCTGAGCTGCGCCATCTGAC 957  
QY 321 AsnTrpGlyHisArgSerAspThrPheValAlaAngIuargGluCysProMetCysBArgThr 340  
Db 958 AGCTGGGCCATGGAGCAGCCATGTCACCTGCTGGCATGTCACGCCAC 1017  
QY 341 ValGlyProTrpValProLeuProLeuGlyCysGluLysIleLeuPheGlyPheTyValPheAla 360  
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QY 361 ProProThrHisAlaPheThrProCysGlyHisValGluLysIleLeuPheGly 380  
Db 1078 CCCCAACTCAGCTTCACCCCTGGGGCACTGCTGTCAGAAGTCTCCAGTGC 1137  
QY 381 TrpSerGlnIleProLeuProIleGlyTyrIleAspAlaPheIleAlaCysProLeuCys 400  
Db 1138 TGTCTGCAGATCCACTGCCACGCGAACCCAGCGTTCTGGCCCTCTGGCT 1197  
QY 401 AlaThrGlnLeuValGlyGluGlnAsnCysIleIleLeuIlePheGlyGlyProLeuCys 420  
Db 1198 GCGACGAGCTGTGGAGAAAGAACTGCACTAATGATTTCCAGGCGCAGGAC 1257  
BC072991 BC072891 1646 bp mRNA linear VRT 03-AUG-2004

DEFINITION	Xenopus laevis MGC80329 protein, mRNA (cDNA clone MGC:80329)
IMAGE	50740481, complete cds.
ACCESSION	BC072891
VERSION	BC072891.1 GI:49119163
KEYWORDS	Xenopus; Xenopus laevis (African clawed frog)
SOURCE	
ORGANISM	Xenopus laevis
AUTHORS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Ripoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
REFERENCE	Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W. and Richardson, P.
JOURNAL	Dev. Dyn. 225 (4), 384-391 (2002)
PUBLISHED	1245917 (bases 1 to 1646)
REFERENCE	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Carninci, P., Prange, C., Raha, S.J., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mullay, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Soerger, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A.C., Young, A.C., Shcherchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Kizyinski, M.I., Skalska, U., Smalius, D.E., Scherzer, A., Schein, J.E., Jones, S.J. and Marras, M.A.
TITLE	Genetic and genomic tools for Xenopus research: The NIH Xenopus Initiative
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBLISHED	1247932
REFERENCE	3 (bases 1 to 1646)
AUTHORS	Klein, S. and Gerhard, D.S.
REMARK	Contact: XGC help desk Email: cgapbs-x@mail.nih.gov Tissue Procurement: Dr. Igor Dawid cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIIL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada inf@bcgsc.ca Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Ancu Petrescu, Anna Liisa Prabhu, Parvaneh Saedi, JR Santos, Angelique Scherzer, Ursula Skalska, Duane Smalius, Jeff Stott, Miranda Tsai, George Yang, Jacqueline Schein, Asim Siddiqui, Rob Holt, Marco Marra.
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIIL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRK plate: 152 Row: h Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
FEATURES	Location/Qualifiers 1. .1646
ORIGIN	
ALIGNMENT SCORES:	
PROT. NO.:	6.84e-155
SCORE:	2138.50
PERCENT SIMILARITY:	96.9%
BEST LOCAL SIMILARITY:	91.2%
DIRECT MATCH:	93.4%
DB:	5
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QY	1 MetPheSsProGlyGlnGluLysCysAlaProAsnLysGluProValLysTyrGly 20
QY	21 GluLeuValValLeuLysTyrArgLysValLeuProLysGlyAspArgLysArgGly 40
QY	396 GAGCTGGGTGTTGCTGCTACAGCGCTGTCCTCAATGGGATCGAGGCCAA 455
DO	336 ATGTTTCCCGAGTCAGGAGCATTCGCCCCAGTAAGGAGCCGGAATAGGA 395
QY	41 SeArgPheAlaLeuThrLysArgProLysAlaArgLysValLeuProSerThrValHis 60
DO	456 AGGAGATTGCACTCTCAAAGGCCAAATCTAACGGGGTAGACGCCAGAGTCAAT 515
QY	61 ValIleSerThrProGlnAlaSerLysValAlaIleSerCysLysArgLysGlnIleSerIleSer 80
DO	516 GIGATTCGACCCGAGCTCCAAAGCCAATCAGCAGAGGCCAACAGCACCTCA 575
QY	81 Tyr-ThrIleSerArgAsnGlnThrValValGlyLysThrHisAspLysAspTAP 100
DO	576 TCAATTCATTCAGAAGCTGAGCTGTTGGTGAATACCCATGAAAGGACAGCTA 635
QY	101 MetPheGlnValGlyArgSerThrGluSerProLeuAspPheValThrAspThrIle 120
DO	636 ARCTTCTGAGATGGAAGCTCAACAGAAAGGCCATCTGACTTGATGACTGATACGGT 695
QY	121 SerGlySerGlnAlaThrAspGluAlaGlnIleThrGlnSerThrIleSerArgPheAla 140
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QY	141 CysArgIleValCysAspArgGluProTyrThrAlaArgIlePheAlaAlaGlyPhe 160
DB	753 TGTAGGATGAGTCGGAAGAACCCGCGTACACAGCTAGATATTGTCAGGATT 812
QY	161 AspSerSerLysAlaIlePheLeuArgYVluLysAlaAlaValIlePheAsnProArgPhe 180
DB	813 GACTCTCTCAAATAATTCTCTGCTGAGAAGCCTCAAGTGGAAAGAATCCTGAGCT 872

ORIGIN	FEATURES	COMMENT	TITLE	JOURNAL	PUBLISHED	REFERENCE	AUTHORS	REMARK
QY	181 HisMetAspGlyLeuThrThrAsnGlyValLeuValMethisProArgGly31PheThr 200						Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Pahey, J., Helton, E., Ketteman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smaklus, D.E., Schnarch, A., Schein, J.B., Jones, S.J. and Marr, M.A.	
QY	201 GluGluSerGlnProGlyValTyrArgGluIleSerValCysIleArgValThrIle 220						Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smaklus, D.E., Schnarch, A., Schein, J.B., Jones, S.J. and Marr, M.A.	
QY	933 GATGAAATCGAGCTGGCTTGCTGTGCAACAGGAACTTTGCGATGTTATACATTA 992						Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
QY	221 ArgGlutGlyArgSerAlaGlnGlyValLeuValGluSerGluThrValLeu 240						Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
Db	993 ArgGluGlyArgSerAlaGlnGlyValLeuValGluSerGluThrValLeu 240						2 (bases 1 to 1936)	
QY	241 GluAspGlySerIleIleLeuLeuIleAspLeuCysGlyIle 260						Klein, S. and Gerhard, D.S.	
Db	1053 CAGGATGGTCCTCTGTCGACTTATGTCGCGCCACCCCTTGCGACAGCGATGG 1112						NIH-MGC Project	
QY	261 LeuPheHisThrProThdIleIleGluIleGluIleArgIleGluIleAla 280						Contact: GGC help desk	
Db	1113 TGTCTCCATAGGCCGACTGCTCAAACACATGGA 1052						Email: cbaps-r@mail.nih.gov	
QY	281 ArgProGlyCysProValGlyLeuAsnThrLeuAlaPheProSerIleAsnArgGlyGlu 300						Tissue Procurement: Robert M. Grainger	
Db	1173 AGGCTTCACTGCCCCTGATTCACCTTCCACATGACCCAGAT 1232						CDNA Library Preparation: Life Technologies, Inc.	
QY	301 ValValGluGluIleGlyGlnProProAlaTyroLeuSerCysGlyGlyValHisGlyTyHis 320						CDNA Library Arrangement: The I.M.A.G.E. Consortium (LNL)	
Db	1233 GTGCTAGAAGACAACAGCTTGCTTACCTCAAGTGTGTCATGTCATCAT 1292						DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada	
QY	321 AsnTrpGlyIleIleArgSerAspThrGluIleArgIleArgGlyCysProMetCysArgThr 340						Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Brown, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Marion, Mike R. Mayo, Josh Moran, Ryan Morin, Terika Olson, Diana Palmquist, Anta Petrecu, Anna Liisa Prabhu, Parvaneh Saedi, JR Santos, Angelique Schnarch, Ursula Skalska, Duane Smilus, Jeff Stort, Miranda Tsai, George Yang, Jacqueline Schein, Asim Siddiqui, Rob Holt, Marco Marras.	
Db	1293 ACTGGGCGAACATGCGAGCACAGCAAGGCAAGAACCGGAGTCCTATGTCAGCA 1352							
QY	341 ValGlyProTyroValProLeuLeuPheGlyCysGlyGluIleGlyPheThrValPhePheAlaGly 360							
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QY	361 ProProThrHisIlePheThrProCysGlyIleValCysSerIleIleSerAlaValThr 380							
Db	1413 CTCCTCTACGCGTTCAAGCTGCGACACTCTCTCTGAAATCTCCAAAT 1472							
QY	381 TRSPeGlnIleProLeuProHisGlyIleIleAlaPheHisIleAlaCysProPheCys 400							
Db	1473 TGGTCCAGATCGCTCCACAGCTACAGCAGCGTTCACCCGCTGCGCTTCCTG 1532							
QY	401 AlaThrGlnIleValGlyIleGluGlnAsnCysValIleLeuIlePheGlyProLeuCys 420							
Db	1533 GCAATCACATTGCTGCGGAGAGAGCTGCTGCAACTTATTCAGGCCCTGTCAC 1592							
RESULT 11								
BC063200	BC063200 1936 bp mRNA linear VRT 23-AUG-2004							
DEFINITION	Xenopus tropicalis hypothetical protein MGC75650, mRNA (cdna clone MGC75650 IMAGE:5379633), complete cds.							
ACCESSION	BC063200							
VERSION	BC063200.1 GI:38649365							
KEYWORDS	MGC.							
SOURCE	Xenopus tropicalis (Silurana tropicalis)							
ORGANISM	Xenopus tropicalis Bukit-Pota, Metacra; Chordata; Craniata; Vertebrate; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Xenopodinae; Xenopus; Silurana.							
REFERENCE	1 (bases 1 to 1936)							
AUTHORS	Strainberg R.L., Feingold E.A., Grouse, L.H., Derge, J.G., Klaunser, R.D., Collins, P.S., Wagner, L., Shemesh, C.M., Schuler, G.D., Altshul, S.F., Zeeberg, B., Butow, K.H., Schneider, C.F., Bhat, N., Hopkins, R.P., Jordan, H., Moore, T., Max, S.I., Wang, J.J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loqueland, N.A., Peters, G.J., Abramson, R.D., Mulahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,							

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Pred. No.:	4.05e-154	Length:	1936			
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Db	365 ArgTrpTrccCACTCAGAGGGACACTCGGCCAGTCAGAGTCATGAAAGCCGAGTCATGTTAGACA 424	Matches:	384			
QY	21 GluLeuValValLeuGlyTyrAlaGlyAlaLeuProAlaGlyAspGlyLysGargLys 40	Conservative:	22			
Db	425 GAGCTGGTGTGCTGGGGTCAACGGCTCTCCAAATGGGAATGAGGATCGAGGAAGGGAA 484	Mismatches:	13			
QY	41 SerArgPheAlaLeuTyroLysGlyProValAlaGlyValLysProSerThrValHis 60	Indels:	1			
Db	485 AGCGAGATTCGACTCTTAAACGCCAAATCCATGGTGGAGCCAGCTCTCC 544	Gaps:	1			
QY	61 ValIleSerThrProGlnAlaSerIleAlaSerCysLysGlyLysSerGluLysSerAlaLysTyr 80					
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QY	81 TyrThrLeuSerArgAsnGlnThrValValGluThrThrIleAspLysAspThreon 100					
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QY	101 MetPheGlnValGlyArgSerThrGluSerProIleAspPheValValThrAspThrIle 120	RESULT 12				
Db	665 ATGTTTCACTATTCAGCAAGTCAGCTGAGCTGTTGTTGTTGTCATGACAGCCT 724	LOCUS	BD190327			
QY	121 SerGlySerGlnAlaThrAspGluLysGlnIleThrGlnSerThrIleSerArgPheAla 140	DEFINITION	BD190327_1 GT:33000066			
Db	725 TCTGGCAACCAAGAT--GATGAAACAGATAACAGAGTACATCTAGATTGG 781	ACCESSION	BD190327_1			
QY	141 CysArgGlyValCysAspArgAspGluProTyroThrIleArgIlePheAlaAlaGlyPhe 160	VERSION	BD190327			
Db	782 TGCGGAGATGCTTGACGAGACCTCTGGTACACGGCTAGATAATTGCTGGAGATT 841	AUTHORS	WO 03008559-A/67.			
QY	161 AspSerSerIleValIlePheLeuGlyGluValAlaAlaSTPLysAsnProAspGly 180	REFERENCE	I (bases 1 to 1717)			
Db	842 GACTCTCTCAAATAATATTCTTGCTGAGAAGGGCCAACTGGAAACATCTGATGGT 901	TITLE	Eki1 phosphorylation related gene			
QY	181 HisMetAspGlyLeuThrThrAspGlyValLeuValMetIleProArgGlyGlyPheThr 200	JOURNAL	Patent: WO 0300858A1, 67 30-JAN-2003;			
Db	902 CATATGGATGGACTRACTACCAATGGGTCTTGATGATCCGAAAGGGTTACT 961	COMMENT	ASAHI KASHI CORP., OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI			
QY	201 GluGluSerGlnProGlyValTtPArgGluIleSerValCysGlyAspValTyrThrIle 220	ORGANISM	Mus musculus (mouse)			
Db	962 GAGAATTCAGGCCTGGGAAATTCTAGCTGTGAGAGTATATACATTA 1021	PD	PN			
QY	221 ArgGluLysArgSerGlnAlaGlnGlyLysLeuValGluSerGluThrAsnValLeu 240	PR	30-JAN-2003			
Db	1022 AGAGAAACGAGCTGCTCAGCAAGGCAACTTGCGAAATGAAACCATATCTG 1081	PR	15-JUL-2002 WO 2002JP007174			
QY	241 GluAspGlySerIleIleAspLeuGlyGlyValLeuLeuItpGlyAlaAspGly 260	PI	18-JUL-2001 JP 01P 218204, 31-AUG-2001 JP 01P 263450 PR			
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QY	261 LeuPheHisThrProThrGlnLysIleGluLeuIleArgGlnGluLeuAlaAla 280	PI	OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI PC			
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QY	281 ArgProGlnCysProValGlyLeuAlaThrLeuLeuItpPheProSerIleAlaGlyGlu 300	CC	Eki1 phosphorylation related gene			
Db	1202 AGGCTCTACTGCGCTGTTGATTAACACTTACTTCTTCCACTATGACCCAAAGT 1261	Key	Patent: WO 0300858A1, 67 30-JAN-2003;			
QY	301 ValValGluGluIleAspGluProTrpAlaTyrLeuSerCysGlyLysValHisGlyTyrIle 320	FT	ASAHI KASHI CORP., OSAMU MATSUZAKI, AKIO MATSUDA, YUKIKO NAGANO, NAOMI SUZUKI			
Db		CDS				
QY	ORIGIN	FEATURES	Location/Qualifiers			
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Db						
QY	Alignment Scores:	Pred. No.:	8.55e-153	Length:	1717	
Db		Score:	21.11.50	Matches:	388	
QY		Percent Similarity:	95.2%	Conservative:	12	
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QY		Query Match:	92.2%	Indels:	1	
Db		DB:	6	Gaps:	1	
QY	US-10-041-030-4 (1-420) x BD190327 (1-1717)					
Db	1262 GTGCTAGAGAGAACGCCCTGGCTTACCTCTACCTGTCATGCCACGGCTATCAT 1321					
QY	321 AsnTRPGLYHISArgSerAspThrGluAlaAsnGluArgGluCysProMetCysArgThr 340					
Db	1322 AACGGGCTCATGCGAGCACAGAGTCATGAAAGCCGAGTCCTGTCATGTTAGACA 1381					
QY	341 ValGlyProTyroValProLeuItpLeuGlyCysGluAlaGlyPheTyrValItpAlaGly 360					
Db	1382 GTGGTCTCTATGCCCCATANGCTTGTGTTGAGAGGATCTAGTACATGCTGAGA 1441					
QY	361 ProProThrHisAlaPheThrProCysGlyHisValCysSerGluLysSerAlaLysTyr 380					
Db	1442 CCTCTACTGCTTAACTCTGGCTGACGCTGCTGCGCTGAAAGCTCTCCAAATAT 1501					
QY	381 TRSPERGlnIleProLeuProHisGlyThrHisAlaPheHisAlaAlaCysProPheCys 400					
Db	1502 TGGCTCAGATTCACTGCCACATGGTACACGGTTCTGCTGCTGCTGCTGCTG 1561					
QY	401 AlaThrGlnLeuValGlyCysLysSerIleLeuIlePheGlnGlyProLeasp 420					
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## ORIGIN

## Alignment Scores:

Pred. No.: 1.67e-144

Length: 2474

Matches: 351

Conservative: 28

Mismatches: 31

Indels: 8

Gaps: 2

US-10-041-030-4 (1-420) x BC075973 (1-2474)

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 Query 21 Glu Leu Val Val Ile Gly Tyr Arg Gly Ala Pro Alanine Glu Pro Alanine Glu Pro Val Lys Tyr Gly 40  
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 Query 41 Ser Arg Phe Alanine Tyr Lys Arg Pro Lys Alanine Glu Pro Alanine Glu Pro Val Lys Tyr Gly 60  
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 Db 61 Val Ile Ser Thr Pro Gln Alanine Ser Lys Alanine Ser Cys Lys Glu Gln His Ser Ile Ser 80  
 Query 398 A T C C T T A C A G C A C C A C A G C C A G G C A G G C A G T G T A A G G C C A G C A C T C T C 457  
 Query 81 Tyr Ile Leu Ser Arg Asn Glu Ile Val Val Glu Thr His Asp Lys Asp Thr Asp 100  
 Db 458 T A C A G C T C T C A G A A C C A G C A C G C T G G T G T G A C G C C A T G A C A A G A C C G A C 517  
 Query 101 Met Phe Gln Val Ily Garg Ser Thr Glu Ser Pro Ile Asp Phe Val Val Threonine Phrile 120  
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 Result 15 AR483566  
 Locus AR483566  
 Definition Sequence 3 from patent US 6703487.  
 Accession AR43566  
 Version AR483566.1 GI:47246650  
 Keywords SOURCE  
 ORGANISM Unknown.  
 Reference Unclassified.  
 1 (base 1 to 1257)  
 Authors Bird, T.A. and Cosman, D.J.  
 Title Human polino polypeptides  
 Journal Patent: US 6703487; A 3, 09-MAR-2004;  
 Immunex Corporation, Seattle, WA;  
 WOX;

FEATURES  
 Source location/qualifiers 1. .1257  
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## ORIGIN

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US-10-041-030-4 (1-420) x AR483566 (1-1257)

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 Qv 21 GluLeuValValLeuGlyTyrArgGlyAlaLeuProArgLysAspArgGlyTyrGly 40  
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 Db 415 TGCGAAATCATATCTGAACTGAACTCTCTTACAGCAGGATTAAGCTGCTCAGGGTT 474  
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 Db 535 CAGATGGATGGCTGACCTAACTGGCTCTTGATCCACGGATGGTTCA 594  
 Qv 201 GluGlusErGlnProGlyValTrpArgGlyIleSerValCysGlyAspValYlTyrThrIeu 220  
 Db 595 GAAGACTCCAAAGCTGGATGAAATGGAGAAATGGTGTGGTGTGGAAATTTAGCCCA 654  
 Qv 221 ArgGluLysArgSerAlaIleGlnGlyLysLeuValGluSerGluThrValIeu 240  
 Db 655 CGTGTAAACCGATCGGCTCAGCAGAGAAATGGTGAATGAAACCATCTAGTTA 714  
 Qv 241 GluAspGlySerIleIleAspLeuCysGlyAlaThrIleLeuTrpThrAlaAspGly 260  
 Db 715 CAAGATGGCTGGTTAATGACACTCTGCTGCTGCAACATGTTATGGCTACTSGAGAGC 774  
 Qv 261 LeuPheHisThrProThrIleBhistileGluIleIleArgGlnGluLeuAlaAla 280  
 Db 775 CTTCCTCAACCTCTACCTGAGCATTTAGCTTAACTGAGCTAGGAACTGCTGCA 834  
 Qv 281 ArgProGlnCysProValGlyLeuAsnThrLeuAlaPheProSerIleAsnArgGlyGlu 300  
 Db 835 CGACCTCACTGCTGCTGAGGTCAACACACTAGCATTTCTAGTAGTGAAGGAGAGAC 894  
 Qv 301 ValValGluGlyIleGlnProTrpAlaIleTyroLeuSerCysGlyLysValHisGlyTyrHis 320

---

DB 895 GTGTAGTGAAACACCACTGGATATCTAACTGGCCATGTCAGTGGCTATCAT 954  
 Qv 321 AenTRPGlyIleArgSerAspThrGluLysAlaLysGluArgGluCysPrometCysArgThr 340  
 Db 955 AACGGGGAAAGAGAACGAGCTGATGCGMAAGATGCTGATGTCCTATGTTGAGCT 1014  
 Qv 341 ValGlyProTyrValProLeuTrpLeuGlyCysGluAlaGlyPhenylTyrValAspAlaGly 360  
 Db 1015 GTGGTCCCTCTGTTCTGAGCTGCTGAGCTGAAAGCTGAGCTGAGCTGCGGC 1074  
 Qv 361 ProProThrHisAlaPheThrProCysGlyHisValCysSerGlyLysSerAlaLysTyr 380  
 Db 1075 CCTCCAAACCCATCGGTTAGCCGTTGGGAGTGTGTTGAAAGAACACTGCCTAT 1134  
 Qv 381 TrpSerGlnIleProLeuProHisGlyTyrThrHisAlaAlaLysCysProProHeCys 400  
 Db 1135 TGCTCCGAGATCCCACTCTCTGCTGAGCTACTCATACTTCTGAGCCGCTGCTTGT 1194  
 Qv 401 AlaThrGlnLeuValGlyCysGlnAspCysIleLysIlePheGlyGlyProLeuAsp 420  
 Db 1195 GCACATGCTTCTGCTGGAACAGGCTCATCAGACTTATTTCAAGGACCTCTAGAC 1254

Search completed: March 2, 2006, 07:33:41.  
 Job time : 6959 secs

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GenCore version 5.1.7

OM protein - protein search, using sw model  
Run on: March 1, 2006, 21:01:56 ; Search time 20 Seconds  
(without alignments)  
418.898 Million cell updates/sec

Title: US-10-041-030-4

Perfect score: 2290

Sequence: I MFSPQQBHQHCPANKEPVKG. .... AQLQVGEONCIRKIQFQSPID 420

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 133702 seqs., 19947517 residues

Total number of hits satisfying chosen parameters: 133702

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1:	/cgn2_6/ptodata/1/pupbaa/US08_NEW_PUB.pop:*
2:	/cgn2_6/ptodata/1/pupbaa/US06_NEW_PUB.pop:*
3:	/cgn2_6/ptodata/1/pupbaa/US10_NEW_PUB.pop:*
4:	/cgn2_6/ptodata/1/pupbaa/PCT_NEW_PUB.pop:*
5:	/cgn2_6/ptodata/1/pupbaa/US109_NEW_PUB.pop:*
6:	/cgn2_6/ptodata/1/pupbaa/US11_NEW_PUB.pop:*
7:	/cgn2_6/ptodata/1/pupbaa/IS11_NEW_PUB.pop:*
8:	/cgn2_6/ptodata/1/pupbaa/US60_NEW_PUB.pop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1482.5	64.7	406	7 US-11-072-512-3928 Sequence 3928, App
2	90	3.9	800	7 US-11-024-959-511 Sequence 511, App
3	90	3.9	984	6 US-10-935-561-62 Sequence 629, App
4	89	3.9	452	7 US-11-087-093-7273 Sequence 7273, App
5	89	3.9	800	7 US-11-024-959-471 Sequence 471, App
6	88	3.8	1345	7 US-11-052-558A-282 Sequence 282, App
7	87.5	3.8	1121	7 US-11-024-959-459 Sequence 459, App
8	87	3.8	320	7 US-11-087-099-7278 Sequence 7278, App
9	87	3.8	2105	7 US-11-052-558A-173 Sequence 173, App
10	86.5	3.8	266	7 US-11-072-512-3891 Sequence 3891, App
11	86	3.8	759	7 US-11-149-003-22 Sequence 22, App
12	86	3.8	1057	7 US-11-149-03-6 Sequence 6, App
13	86	3.8	1192	7 US-11-145-003-18 Sequence 18, App
14	86	3.8	1207	7 US-11-149-003-20 Sequence 20, App
15	86	3.8	1251	7 US-11-149-03-16 Sequence 16, App
16	86	3.8	1342	7 US-11-149-003-24 Sequence 24, App
17	86	3.8	1477	7 US-11-149-003-8 Sequence 8, App
18	86	3.8	152	7 US-11-149-003-1 Sequence 10, App
19	86	3.8	1535	7 US-11-145-003-14 Sequence 14, App
20	86	3.8	1570	7 US-11-149-003-12 Sequence 12, App
21	86	3.8	1593	7 US-11-149-003-16 Sequence 4, App
22	86	3.8	1628	7 US-11-149-003-2 Sequence 2, App
23	86	3.8	2176	7 US-11-193-561-25 Sequence 25, App
24	86	3.8	2176	7 US-11-193-771-25 Sequence 25, App
25	86	3.8	2176	7 US-11-193-789-25 Sequence 25, App

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Sequence 25,	Appl
Sequence 38,	Appl
Sequence 2,	Appl
Sequence 633,	App
Sequence 23,	Appl
Sequence 23,	Appl
Sequence 23,	Appl
Sequence 21,	Appl
Sequence 21,	Appl

US-11-072-512-3928  
Sequence 3928, Application US/11072512  
Publication No. US20060029945A1  
GENERAL INFORMATION:  
APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHI, SHIZURO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, TUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIBE, RIOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOKO  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKI  
APPLICANT: NAGHARI, KENJI  
APPLICANT: MASUJO, YASURO  
TITLE OF INVENTION: Novel full length cDNA  
FILE REFERENCE: 084135-0191  
CURRENT APPLICATION NUMBER: US/11/072,512  
CURRENT FILING DATE: 2005-03-07  
PRIOR APPLICATION NUMBER: US 60/350,978  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: JP 2001-379298  
PRIOR FILING DATE: 2001-11-05  
NUMBER OF SEQ ID NOS: 4096  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3928  
LENGTH: 406  
TYPE: PRT  
ORGANISM: Homo sapiens  
;  
US-11-072-512-3928

Query Match 64.7%; Score 1482.5  
Best Local Similarity 65.6%; Pred. No. 4  
Matches 275; Conservative 36; Mismatched 0

3 SPGQHEHCAPKNEPVKGHLVVLGVGNGALPNC  
||| :||:|||  
30 SPG-EDAGPGEEPKYGBL-  
63 STPOQSKATCKGKHISYTLSRNQTVWVBYT

Db 49 STPLVSKAISNRGHSISYTSLRSHSVIVETYHSDTMFQGRSTERMIDFVFTDPSG 108

Qy 123 SQNDEAOITQSTSISRFACRIVCDRNEPYTARIFAGDSSKNTFLGEAKKWNPHM 182  
Db \* 109 G-GAEGRSAQSITSRVACRILCDRRPPTARYAAGDASMSFLGERAAKRTPOGM 167

Qy 183 DGLUTINGLVMHPRGPFTEESQPGWREISVCGDVYTRETRSAQORGKLVSEENVQD 242  
Db \* 168 DGLUTINGLVMHPGGFSPSDASCPWREISVCGVYTRDSRQAQRKLVSEENVQD 227

Qy 243 GLSLDLCGATLMLRTADGLFLHTPROKHLBALROBINAARPOCPVGLNLAPPSINRKEW 302  
Db 228 GSLDLCGATLMLRTAPGLRAPIKLOLAQRORANARPOCPVGLSLAFFSPARGRTA 287

Qy 303 BEK-QPWTALSCGHVHGTYHNGHRSDEANERCPMCITVGVPGVPLMGCBGPFVUDGP 361  
Db 288 PDIQQPWVYVRCGTVHGVGCRERGQRCPLCIVGVPGVPLWQEDAGLCPGP 347

Qy 362 PTAFTPCCHVCSEKSIAKWSQIPPLPHGTHAFHACPPCATQIVGEONCIKJLFQGPID 420  
Db 348 PSHAFAPOGHVCSEKTRYWAQTPPLPHGTHAFHACPPGAUTGEHCVRUJFQGPID 406

RESULT 2  
US-11-024-959-511

; Sequence 511, Application US/11024959  
; Publication No. US200601010516A1

; GENERAL INFORMATION:  
; APPLICANT: RICHARD L.

; APPLICANT: CONNETT, MARIE B.  
; APPLICANT: EMERSON, SARAH JANE  
; APPLICANT: GRIGOR, MURRAY ROBERT  
; APPLICANT: HIGGINS, COLLEEN M.  
; APPLICANT: LUND, STEVEN TROY  
; APPLICANT: MAGUSIN, ANDREAS  
; APPLICANT: KODRZYCKI, BOB

; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS  
; FILE REFERENCE: 044633060  
; CURRENT APPLICATION NUMBER: US/11/024,959

; CURRENT FILING DATE: 2004-12-30  
; PRIOR APPLICATION NUMBER: 60/533,036

; PRIOR FILING DATE: 2003-12-30  
; NUMBER OF SEQ ID NOS: 792  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 511  
; LENGTH: 800

; TYPE: PRT  
; ORGANISM: Pinus radiata  
; US-11-024-959-511

Query Match 3.9%; Score 90; DB 7; Length 800;  
Best Local Similarity 26.4%; Pred. No. 3.6; Mismatches 9; Indels 59; Gaps 6;

Matches 46; Conservative 9; Mismatches 59; Indels 60; Gaps 6;

Qy 47 KRKGANGYKPRSTHVISTPQ-ASKAISCKG-----QHHS-----YT 82  
Db 351 KEPKTTISLTTPGGLSSPQRAGIAFSSKLPASSGPPSYVSPKKOUSTSRQPTTNPQT 410

Qy 83 LSRNQTVVV-----EYTKDTDMFOQGRSTESPIDFVVTDTISGSQNTDE---- 128  
Db 411 LSRPDIVPVIVPRNSLRPETSDAKKEMANFGRVVPSTVTKSGSNRDES DKI 470

Qy 129 -----AOITOSTISR---ACRVCDRNEPYTARIFAGP 160  
Db 471 DSIQNKRMTGNDKTDINTJARAEQVSSRUDNTNTSSVCDGQPAARWGAAC 524

Query Match 3.9%; Score 89; DB 7; Length 452;  
Best Local Similarity 22.1%; Pred. No. 2; Mismatches 149; Indels 98; Gaps 14;

Matches 79; Conservative 32; Mismatches 149; Indels 98; Gaps 14;

Qy 48 RPKANGYKPRSTHVISTPQASKAISCKGQHSISYTSLRSHSVIVETYHSDTMFQGRSTERMIDFVFTDPSG 108  
Db 51 RKQAVLIGPSANRVLVQEAMNSRIGWYFIESTGNTNTLQDGSRBRRLTRMLYPAPH 110

; GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CJO01559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FastqSEQ for Windows Version 4.0

SEQ ID NO 629

LENGTH: 984

TYPE: PRT

; ORGANISM: Homo sapiens  
; US-10-995-561-629

Query Match 3.9%; Score 90; DB 6; Length 984;

Best Local Similarity 19.4%; Pred. No. 4.9; Mismatches 119; Indels 160; Gaps 23;

Matches 79; Conservative 49; Mismatches 119; Indels 160; Gaps 23;

Qy 3 SPCQEBEHCAPIKEPVKVGELVVLGYNGALPNQDRGRRSREALYKOPK----- 50  
Db 619 TPSQ-----PNSHPIQW-----NAPQPSHISKVILRMPKNSVGRWKBAITP 660

Qy 51 -----ANGVKPSTVH---VISTPORKSKATCKGHSIS--YTISRNQTVVETHDK 97  
Db 661 GHLSNYTTKGKLGPKGVVYEGOLISIQ-----YGHQEVTRDPFTTISTTPVTSVTVG 713

Qy 98 DTMFMQVGRSSTSP-----DFVW-----IDTISG-----SQWDEAOITQ--STIS 137  
Db 714 BTTPSPRSPRIVATEVTTASSFRVWSNSADTVESEFRVETSDPDTYDPLSPAT 773

Qy 138 RFACTRIVDRNRP-----YTAIRAGFDSSKNTFL--GEKAALKWNPDCHMDGTTN 188  
Db 774 SV-----NPDLLRCKVIVVVOISEDGEQSLISTSQTADAPPRTVQDVT 825

Qy 189 GVLMHPR-----GQFT-----ESOPGWMRIBISVCGDVY 218  
Db 826 SIVVRWSRSPQAPITGIRIVVSPSVEGSSTEALNPETANSVTLSDLOPQVQNTI--IY 881

Qy 219 TURETRRA-----Q-----RGKLYESTENYIQLQESLIDICGATLWRTRADLFLHTPTQ 267  
Db 882 AVENQNSTSPVVIQETTGTPSPSDTVPSPRD-LQFVETDVLKVTRMM-----TPE 931

Qy 268 KHIALRQEINAAR-----POCPVGLNLAPPSINRKEVVEBKQW 308  
Db 932 SAVTGYRVDVIVPNLPGEEHGQRLPISNTLC-----SEPW 966

RESULT 4  
US-11-087-099-7273

; Sequence 7273, Application US/11087099  
; Publication No. US20060041961A1

; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.

; TITLE OF INVENTION: Genes and Uses for Plant Improvement

; FILE REFERENCE: 38-21(53450)B EP 11/087,099

; CURRENT APPLICATION NUMBER: 2005-03-22

; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464

; SEQ ID NO 7273  
; LENGTH: 452

; TYPE: PRT

; ORGANISM: Nobotoc punctiforme  
; US-11-087-099-7273

Query Match 3.9%; Score 89; DB 7; Length 452;

Best Local Similarity 22.1%; Pred. No. 2; Mismatches 149; Indels 98; Gaps 14;

Matches 79; Conservative 32; Mismatches 149; Indels 98; Gaps 14;

Qy 48 RPKANGYKPRSTHVISTPQASKAISCKGQHSISYTSLRSHSVIVETYHSDTMFQGRSTERMIDFVFTDPSG 108  
Db 51 RKQAVLIGPSANRVLVQEAMNSRIGWYFIESTGNTNTLQDGSRBRRLTRMLYPAPH 110

; GENERAL INFORMATION:

RESULT 3  
US-10-995-561-629

; Sequence 629, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:

QY 87 -----QTVVVEYTHD-KOTDMQVGRTESPIDFVVVTDTISGSONTDEAQITOS 134

Db 111 GKAIAATYPTDTONIVQDFLKDMEGRTISLNFSRQLTMINTRFLGSQNKEVE--- 166

QY 135 T-SRFACRIVCDRNEPYTARIFAGPDSKNTFLGEKAKWNP-DGRNDGJTGTYLM 193

Db 167 -----QTSQWFTQQLDSSMAYT-----KWNVPFTLJGRGMNARGKLV 204

QY 194 HRRGGFTEESQPMRETSVCCGIVYLTRETRASQQRCKLVESTEINVLQDGSLIDCG--- 250

Db 205 FLREATAQRIEBCONLESK--DVLGLIAAVDEDGKL--S-TOVINEALILLFAGHET 259

QY 251 -ATLILWRTADGIFTPTOKHIEALRQEINAARPQCPCVGLNL-AFPST-NRKEVERKOP 307

Db 260 T-SLTLTWIFELNHPEWR--EPRLQEQPLAVVNPNLSHKQFPOITNUKEAERLYP 317

QY 308 WAYLSCGHVHGYNWGRSDTEANERECPCMTRVGPVYPLWLGCEASGPYVDAQPP-TH 364

Db 318 PWYA-----YNRGVLKDIKEYGYRIP-----AGWFVTSPMLTH 351

RESULT 5  
US-11-024-959-471

; Sequence 471, Application US/11024959

; Publication No. US2006010516A1

; GENERAL INFORMATION:

; APPLICANT: FORSTER, RICHARD L.

; APPLICANT: CONNETT, MARIE B.

; APPLICANT: EMERSON, SARAH JANE

; APPLICANT: GRIGOR, MURRAY ROBERT

; APPLICANT: HIGGINS, COLLEEN M.

; APPLICANT: LUND, STEVEN TROY

; APPLICANT: MAGUSIN, ANDREAS

; APPLICANT: KODRZICKI, BOB

; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS

; FILE REFERENCE: 04463-0360

; CURRENT APPLICATION NUMBER: US/11/024, 959

; PRIORITY FILING DATE: 2004-12-30

; PRIOR APPLICATION NUMBER: 60/533, 036

; PRIOR FILING DATE: 2003-12-30

; NUMBER OF SEQ ID NOS: 782

; CURRENT APPLICATION NUMBER: US/11/024, 959

; LENGTH: 800

; TYPE: PRT

; ORGANISM: Pinus radiata

US-11-024-959-471

Query Match 3.9%; Score 89; DB 7; Length 800;  
Best Local Similarity 26.4%; Pred. No. 4.5; Mismatches 9; Indels 6; Gaps 6;  
Matches 46; Conservative 9;

QY 47 KRPKANGVKPSTPVHVISPTQ-ASKAISKG-----OHSIS-----YT 82

Db 351 KEPKTTISLTTEGLISSITPORGATAFSSKLNAPASSGPSYVSTPKKNSTSRVQOPTNWQT 410

QY 83 LSPNQTVWV-----EYTKDPTMFQGRSTESPIDFVPTDRISGNTDE--- 128

Db 411 LSPRDIVPVIVPRNSLRPETSDVKEMNNRERVVFSTVSKTDVWKSGNRDESDFKI 470

QY 129 -----AQITOSTISPF---ACRVCDRNEPYTARIFAGP 160

Db 471 DSINQKRMGTGNDKDLNTARAEGHVSSRLNDNTISSVCDGKQPAARWIGAKF 524

RESULT 6  
US-11-052-554A-282

; Sequence 282, Application US/11052554A

; Publication No. US2005028866A1

; GENERAL INFORMATION:

; APPLICANT: Schdeva, et al.

; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

FILE REFERENCE: 30853/40359A

CURRENT APPLICATION NUMBER: US/11/052, 554A

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589, 227

PRIOR FILING DATE: 2004-07-20

NUMBER OF SEQ ID NOS: 763

SEQ ID NO 282

LENGTH: 1345

TYPE: PRT

ORGANISM: Escherichia coli 0157:H7

US-11-052-554A-282

Query Match 3.8%; Score 88; DB 7; Length 1345;

Best Local Similarity 22.6%; Pred. No. 12; Mismatches 87; Indels 80; Gaps 13;

Matches 58; Conservative 32; No. 12; Mismatches 87; Indels 80; Gaps 13;

QY 50 KANGVKPSTVHVISPTQSKAISCKGHSISYTSRNQ-----VVVEY 93

Db 90 QANG-----BAHV-----TLKGKKA-----GTHIVATLSNNNTSDSQVTPVADKTSALVLIQI 139

QY 94 TRNDKT-----DMEQVERSTESPIDFVDT-----LGSQNTDEAQITQST 135

Db 140 SKNEITENGVDASLTATVKQDFD-NEVNVLNPVTFESTASSGLTLPQESNTNEGIAQT 198

QY 136 ISRFACRIVCDRNEPYTARIFAGFDSSSKNT-FLGEKAKW-----KNP 178

Db 199 LAG-----VAREGQTVIASLANGASDVKTHFEGDAAKIELTPVVDLSIAGTQNS 253

QY 179 DGHM-----DGLTGVLNMHPRGCFTEBSQPG----VREBISVGDVUTLRETSAQ 227

Db 254 SSVITMTVVDNGFPVKGTVNFTSNATAEWINGQAVNBQGKAVVTT-NIRSSI 311

QY 228 QCKQLVSESTNLQDG 244

Db 312 ESGARPDTVEASLNGS 328

RESULT 7  
US-11-024-959-459

; Sequence 459, Application US/11024959

; Publication No. US2006010516A1

; GENERAL INFORMATION:

; APPLICANT: FORSTER, RICHARD L.

; APPLICANT: CONNETT, MARIE B.

; APPLICANT: EMERSON, SARAH JANE

; APPLICANT: GRIGOR, MURRAY ROBERT

; APPLICANT: HIGGINS, COLLEEN M.

; APPLICANT: LUND, STEVEN TROY

; APPLICANT: MAGUSIN, ANDREAS

; APPLICANT: KODRZICKI, BOB

; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS

; FILE REFERENCE: 04463-0360

; CURRENT APPLICATION NUMBER: US/11/024, 959

; LENGTH: 1121

; TYPE: PRT

; ORGANISM: Pinus radiata

US-11-024-959-459

Query Match 3.8%; Score 87.5; DB 7; Length 1121;

Best Local Similarity 20.9%; Pred. No. 10; Mismatches 143; Indels 175; Gaps 27;

Matches 98; Conservative 53; Mismatches 143; Indels 175; Gaps 27;

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

Query Match 3.8%; Score 87.5; DB 7; Length 1121;

Best Local Similarity 20.9%; Pred. No. 10; Mismatches 143; Indels 175; Gaps 27;

Matches 98; Conservative 53; Mismatches 143; Indels 175; Gaps 27;

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

Query Match 3.8%; Score 87.5; DB 7; Length 1121;

Best Local Similarity 20.9%; Pred. No. 10; Mismatches 143; Indels 175; Gaps 27;

Matches 98; Conservative 53; Mismatches 143; Indels 175; Gaps 27;

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

Query Match 3.8%; Score 87.5; DB 7; Length 1121;

Best Local Similarity 20.9%; Pred. No. 10; Mismatches 143; Indels 175; Gaps 27;

Matches 98; Conservative 53; Mismatches 143; Indels 175; Gaps 27;

TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL

Db 207 PNCARTRPQPTASIGVULPCTTTPGPHGPPSSSTATSGLASMSNSNMMTSQPAPY 266  
 Qy 71 ISCKQHSISYTLSRNQTVWVETHDKDTDMFOVGSRSTESPIDFWVTDTIS 123  
 Db 267 V-----GPSVPVNQATLKR-----RTPGSSSVVDYQQTADSEOLIKRLRPS 312  
 124 QNTDEA-----QTQSP-----ISRFACRIVCDRNPYTRIFANGFDSSKNFL-----GEKA 172  
 Qy 313 QSIDEA-----QTQSP-----ISRFACRIVCDRNPYTRIFANGFDSSKNFL-----GEKA 172  
 Db 173 AK-----WNPDGHMDGLTINGVLM-----HPRGGFTESQPGWREISVCGDWYLRE 222  
 Qy 368 GETLWE-----VGSREKLATSFKIQWANDMANGSNHLBAAFKDSSVNR----- 412  
 Db 223 TRSAQQRKLVESBTNVL-----QDSNLIDCGATLWRADGCLFHPTOKHTEALRQ-----EIN 278  
 Db 413 -----VLMSPDGTLIGIA-----FTKHLVHTYTFQGLD-LRQHLEID 448  
 Qy 279 AACRQCPCPVGLNTIAPPSSIRKVEEVKEKQPAVLYCQH-----VHG-----YNGWHR 326  
 Db 449 AH-----VSGVNDLAFLRFSPNPKLCV-----VTCGDDMKVMDAUGTERKLYNFEGHDA 496  
 327 DTEANERECP-----MCRTGGPYVPLWLGCBAFGFYVDAGPPTAFTPCGAWSCEKS 377  
 Db 497 PVVS-----VCPHHKEMIQFSTANDGKIKAWLYDHLGRSYDAP-----GHSCT--- 543  
 Qy 378 AKWSQIPLPHGTHFAACPPCATOLVGE-----ONCIKILFOG 417  
 Db 544 -----TMYSADGTRLFS-----CGSKEGESFLVERNESEGAIKRTYSG 583

RESULT 8  
 US-11-087-039-7278  
 ; Sequence 7278, Application US/11087099  
 ; Publication No. US20060041961A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abad, Mark S. et al.  
 ; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
 ; FILE REFERENCE: 38-21(5450)B EP  
 ; CURRENT APPLICATION NUMBER: US/11/087,099  
 ; CURRENT FILING DATE: 2005-03-22  
 ; NUMBER OF SEQ ID NOS: 12464  
 ; SEQ ID NO: 7278  
 ; LENGTH: 320  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(320)  
 ; OTHER INFORMATION: unsure at all xaa locations  
 ; US-11-087-039-7278

Query Match 3.8%; Score 87; DB 7; Length 2105;  
 Best Local Similarity 22.9%; Pred. No. 27; Mismatches 56; Conservative 35; Indels 86; Gaps 17; Matches 56; Gaps 17;

Qy 4 PGQEBERCAPVKEPVVKYGLVULGVINGALPNS-DRGRKRSRPARLYKRPKANGVKPSTVHV- 61  
 Db 714 PGGDHYAVMISKTGTAGWDFTVFE-----TPNCINKG-----GARFGL-----STEAMAKPOSWIE 767

Qy 62 -----ISTQOASKISCKQOH-----SISYTSRQNQTVVETHDKDTDMFOVGSRSTESPIDFWVT 117  
 Db 768 RIVDULPAGTKVAFRHYNCSDLNVL-----LDIQTIMGGS-----PTPDIYTT 813

Qy 118 DTISSONTDEAQTOQTOSTIERFACRIVCDRNPYTRI-FAG-----FD 161

Db 814 VYRDGTRIKE-----GLTETTFSBDG-----VATSGHEYCVKTAGVSPEKCVTVDPVQFN 868

Qy 162 SSKNI-----FLEGKAA-KWKOPDHMDGLTINGVLMWHPRGFT-----EESQPGWREI 211  
 Db 869 PVQNLJLGSAYQKVTKWQDANG-----TPN-----PNPGTTLESFENGIPASWKI 917

Qy 87 NGALPNGDRGRKSRPFLYKRPKANGVKPSTVHVSTPQASK-ATSKQHSISYTLRN 86  
 Db 11 NLRLPPEPSSRRPRPFLPLPPTTAKPSAGDTIASADLKLAVLGHNGNGTVKV-RH 69

Qy 28 NGALPNGDRGRKSRPFLYKRPKANGVKPSTVHVSTPQASK-ATSKQHSISYTLRN 86  
 Db 70 KTISATYA-----LKIHS-----ADATTRRRASETSLRRASTD----- 106

Qy 145 CDRNPYTYARTIFAACFDSSKNIFLGEKAQKWNPG-----HNDGLTINGVLMWHPRG 197

Db 107 -----PHVVRPHGS-----FENPGDVALTMEYMDGGTUEITALA-TGG 143

RESULT 9  
 US-11-052-554A-173  
 ; Sequence 173, Application US/11052554A  
 ; Publication No. US20050288666A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sachdeva, et al.  
 ; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE PROTEINS OF THERAPEUTIC POTENTIAL  
 ; FILE REFERENCE: 30853-4059A  
 ; CURRENT APPLICATION NUMBER: US/11/052,554A  
 ; CURRENT FILING DATE: 2005-02-07  
 ; PRIOR APPLICATION NUMBER: US 60/1589, 227  
 ; PRIOR FILING DATE: 2004-07-20  
 ; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
 ; PRIOR FILING DATE: 2004-02-06  
 ; NUMBER OF SEQ ID NOS: 763  
 ; SOFTWARE: Patentin version 3.3  
 ; SEQ ID NO: 173  
 ; LENGTH: 2105  
 ; TYPE: PRT  
 ; ORGANISM: Porphyromonas gingivalis W83  
 ; US-11-052-554A-173

Query Match 3.8%; Score 87; DB 7; Length 2105;  
 Best Local Similarity 22.9%; Pred. No. 27; Mismatches 56; Conservative 35; Indels 86; Gaps 17; Matches 56; Gaps 17;

Qy 4 PGQEBERCAPVKEPVVKYGLVULGVINGALPNS-DRGRKRSRPARLYKRPKANGVKPSTVHV- 61  
 Db 714 PGGDHYAVMISKTGTAGWDFTVFE-----TPNCINKG-----GARFGL-----STEAMAKPOSWIE 767

Qy 62 -----ISTQOASKISCKQOH-----SISYTSRQNQTVVETHDKDTDMFOVGSRSTESPIDFWVT 117  
 Db 768 RIVDULPAGTKVAFRHYNCSDLNVL-----LDIQTIMGGS-----PTPDIYTT 813

Qy 118 DTISSONTDEAQTOQTOSTIERFACRIVCDRNPYTRI-FAG-----FD 161

Db 814 VYRDGTRIKE-----GLTETTFSBDG-----VATSGHEYCVKTAGVSPEKCVTVDPVQFN 868

Qy 162 SSKNI-----FLEGKAA-KWKOPDHMDGLTINGVLMWHPRGFT-----EESQPGWREI 211  
 Db 869 PVQNLJLGSAYQKVTKWQDANG-----TPN-----PNPGTTLESFENGIPASWKI 917

Qy 212 SVCGL 216  
 Db 918 DADGD 922

RESULT 10  
 US-11-072-512-3891  
 ; Sequence 3891, Application US/11072512  
 ; Publication No. US2006029945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ISOGAI, TAKAO  
 ; APPLICANT: SUGIYAMA, TOMOYASU  
 ; APPLICANT: OTSUJI, TETSUJI  
 ; APPLICANT: WAKAMATSU, AI  
 ; APPLICANT: SATO, HIROYUKI  
 ; APPLICANT: ISHII, SHIZUKO  
 ; APPLICANT: YAMAMOTO, JUN ICHI  
 ; APPLICANT: ISONO, YUKO



RESULT 13  
 US-11-149-003-18  
 ; Sequence 18, Application US/11149003  
 ; Publication No. US2006014277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walkie, D. Wade  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; TITLE OF INVENTION: Novel Human Kielin-like Proteins and Polynucleotides Encoding the  
 ; FILE REFERENCE: LEK-0360-USA  
 ; CURRENT APPLICATION NUMBER: US/11/149, 003  
 ; CURRENT FILING DATE: 2005-06-09  
 ; PRIORITY APPLICATION NUMBER: US/10/189, 971  
 ; PRIORITY FILING DATE: 2005-06-09  
 ; PRIORITY APPLICATION NUMBER: US 60/302, 949  
 ; PRIORITY FILING DATE: 2005-07-03  
 ; PRIORITY APPLICATION NUMBER: US 60/315, 634  
 ; PRIORITY FILING DATE: 2005-08-29  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 18  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 ; US-11-149-003-18

Query Match 3.8%; Score 86; DB 7; Length 1192;  
 Best Local Similarity 20.5%; Pred. No. 15; Mismatches 120; Indels 100; Gaps 17;  
 Matches 64; Conservative 28; Mismatches 120; Indels 100; Gaps 17;

Qy 166 IFLGEKAAKWKNP----DGHMDGL-----TTNGVLYMHPRGF----T 200  
 Db 896 VLLGDMAVRLLQDGAVTDGHPVALPFLOBLPLYVELRAGHTVILHAQPGLOVLDGGSQV 955  
 Qy 201 EESQPGWM--REISVCGDVYTLRETRSAQQRKLVSEBTNVLQDSLIDLCATLRTA 258  
 Db 956 EVSVPGSYQGRTCGLCNGNFGFAODDQCGPEGSLILSEAAQNS-----WQVS 1003  
 Qy 259 DGLP--HPTPTQKTEARLQEINARFCOPCPVSLNTLAPPSTIRKEYEKOP-----WA 309  
 Db 1019 EGLWPGRPCSAGREVDRPCRAAGYTRARRANARCGVLUKSPFSRCHA VVPPPEPPFAACVYD 1078  
 Qy 310 YLSCGHVGHGHNWHRSDT--EANERECPCMCRTVGPVPLW-----LGC--EAGFVV 357  
 Db 1131 DECGPPCRTCFCNQHPIPLGELAAHCVRCPVPGC-----QCPAGLVEHEAHCIPEA 1181  
 Qy 397 CPFCATOLVGEQ 408  
 Db 1182 CP--QVLLTGQ 1191

RESULT 15  
 US-11-149-003-16  
 ; Sequence 16, Application US/11149003  
 ; Publication No. US2006014277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walkie D. Wade  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; TITLE OF INVENTION: Novel Human Kielin-like Proteins and Polynucleotides Encoding the  
 ; FILE REFERENCE: LEK-0360-USA  
 ; CURRENT APPLICATION NUMBER: US/11/149, 003  
 ; CURRENT FILING DATE: 2005-06-09  
 ; PRIORITY APPLICATION NUMBER: US/10/189, 971  
 ; PRIORITY FILING DATE: 2005-07-03  
 ; PRIORITY APPLICATION NUMBER: US 60/302, 949  
 ; PRIORITY FILING DATE: 2005-07-03  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; US-11-149-003-20  
 ; Sequence 20, Application US/11149003  
 ; Publication No. US2006014277A1

; SEQ ID NO: 16  
; LENGTH: 1251  
; TYPE: PRT  
; ORGANISM: homo sapiens  
; US-11-149-003-16

Query Match 3.8%; Score 86; DB 7; Length 1251;  
Best Local Similarity 20.5%; Fred. No. 16; Mismatches 120; Indels 100; Gaps 17;  
Matches 64; Conservative 28; Mismatches 120; Indels 100; Gaps 17;

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Qy  166  IFLGSEKAAKWKNP-----DGMMDGL-----TTNGCVLVMMPRGCF-----T 200
Db  955  VLGDMAVRLQDGAVTVDSHPVALPFQBLPLVFLRGLHTVILHAQPGLOVLMGDQSV 1014
Qy  201  EESOPCGW--REISVCGDVYLTRLRENSAQORGKVESETNVLQPSLNLICGATLWRRA 258
Db  1015  EVSVPGSYOCRTCGLLCGNFNGPAQDLQCPREGLIPSEAFGNS-----WQVS 1062
Qy  259  DGLP--HPTQKHEALRQEINARPOCPVGLNTLAFFSINRKVEEKQP-----WA 309
Db  1063  EGLAPGRPCSAGGREVPCTRAAGYARREANARCGVLUKSPPSRCHAWPPEPFAACVYD 1122
Qy  310  YLSCHRVHGVNHNGRSDT--EANERECPCMRTVGPVYPLW-----LG---EAGFTV 357
Db  1123  LCACGP-----GSSADACLDALEAYASHCROAG-VIPTWRCPTLCVGCPLERGFV 1174
Qy  358  D-ACPP-----THAFTPGHVCBKSAYKWSQPLPHTAHIA---A 396
Db  1175  DECGPPCPRTFCNOHPLGELAAHCVRPCVPGC-----OCPAGLVTEHEAHCIPPEA 1225
Qy  397  CPFCATQLYQEQ 408
Db  1226  CP--QVLLRSDQ 1235

```

Search completed: March 1, 2006, 21:04:59  
Job time : 21 sec

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GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 1, 2006, 21:01:01 ; Search time 167 Seconds

Sequence: 1 MFSPGQEBEHCAPNPKPVKG.....ATOLVGEONCIKLIPOGHID 420

Title: US-10-041-030-4

Perfect score: 2290

Sequence: 1050.828 Million cell updates/sec

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications AA\_Main:  
 1: /cgn2\_6/ptodata/1/pubbaa/us07\_pubcomb.pep:  
 2: /cgn2\_6/ptodata/1/pubbaa/us08\_pubcomb.pep:  
 3: /cgn2\_6/ptodata/1/pubbaa/us09\_pubcomb.pep:  
 4: /cgn2\_6/ptodata/1/pubbaa/us10\_pubcomb.pep:  
 5: /cgn2\_6/ptodata/1/pubbaa/us11\_pubcomb.pep:  
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 11: /cgn2\_6/ptodata/1/pubbaa/us16\_pubcomb.pep:  
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 40: /cgn2\_6/ptodata/1/pubbaa/us45\_pubcomb.pep:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## Result No.

## Score

## Query

## Match

## Length

## DB

## ID

## Description

## Sequence 1, Appli

## Sequence 2, Appli

## Sequence 3, Appli

## Sequence 4, Appli

## Sequence 5, Appli

## Sequence 6, Appli

## Sequence 7, Appli

## Sequence 8, Appli

## Sequence 9, Appli

## Sequence 10, Appli

## Sequence 11, Appli

## Sequence 12, Appli

## Sequence 13, Appli

## Sequence 14, Appli

## Sequence 15, Appli

## Sequence 16, Appli

## Sequence 17, Appli

## Sequence 18, Appli

## Sequence 19, Appli

## Sequence 20, Appli

## ALIGNMENTS

RESULT 1  
 US-10-041-030-4  
 Sequence 1, Application US/0041030  
 Publication No. US2002015093A1  
 GENERAL INFORMATION:  
 APPLICANT: Powers, Scott  
 APPLICANT: Mu, David  
 APPLICANT: Xiang, Phil.  
 APPLICANT: Peng, Yue  
 APPLICANT: Tularik Inc.  
 TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian Tissue of Invention: Peptide Polypeptides and Polymeric Nucleotides  
 FILER REFERENCE: 018781-005610US  
 CURRENT APPLICATION NUMBER: US/10/041-030  
 PRIOR APPLICATION NUMBER: US 60/259,502  
 PRIOR FILING DATE: 2001-01-02  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn ver. 2.1  
 SEQ ID NO 4  
 LENGTH: 420  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: human pellino 2  
 US-10-041-030-4  
 Query Match Similarity 100.0%; score 2290; DB 4; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-216; Gaps 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 420; Conservative 0;  
 Conservativeness 0;  
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 Sequence 4, Appli  
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 Sequence 7, Appli  
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 Sequence 61, VISTPOASKAISCKGONISIYTSLRNGTWWYTHDKDTDMQVGRTSTESPIDFWMTI 120  
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 181 HMDGLITTGVLVWMPGGFTERSQPGWRELSVCGDVTIRETRSAQRGKVVESEINVL 240  
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RESULT 2  
US-10-197-666A-116  
Sequence 136, Application US/1019766A  
Publication No. US20030092037A1  
GENERAL INFORMATION:  
APPLICANT: ASAMI KASEI KABUSIKI KAISHA  
TITLE OF INVENTION: eki phosphorylation related gene  
FILE REFERENCE: PH-1548JS

CURRENT APPLICATION NUMBER: US/10/197, 666A  
CURRENT FILING DATE: 2002-11-18  
PRIOR APPLICATION NUMBER: JP 2001-218204  
PRIOR APPLICATION NUMBER: JP 2001-263450  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: JP 2002-012176  
PRIOR FILING DATE: 2002-01-21  
PRIOR APPLICATION NUMBER: US 60/105, 884  
PRIOR FILING DATE: 2001-07-18  
PRIOR APPLICATION NUMBER: US 60/316, 304  
PRIOR FILING DATE: 2001-09-04  
PRIOR APPLICATION NUMBER: US 60/350, 027  
PRIOR FILING DATE: 2002-01-23  
NUMBER OF SEQ ID NOS: 156  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 136  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-197-666A-116

Query Match 100.0%; Score 2290; DB 4; Length 420;  
Best Local Similarity 100.0%; Pred. No. 1; gape 0;  
Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFSPGQEEHCAPNKEPVKYGELVWYNGALPNCDRGRKRKFALYKRPKANGVKSTVH 60  
Dy 1 MFSPGQEEHCAPNKEPVKYGELVWYNGALPNCDRGRKRKFALYKRPKANGVKSTVH 60

Qy 61 VISTPOASKAISCKGHOHSISYTLRSNOTWVYTHDKDTDFQVGISTTESPIDEFVTTI 120  
Dy 61 VISTPOASKAISCKGHOHSISYTLRSNOTWVYTHDKDTDFQVGISTTESPIDEFVTTI 120

Qy 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYTRIFAGPSSKNFLGEAKWKPDG 180  
Dy 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYTRIFAGPSSKNFLGEAKWKPDG 180

Qy 181 HMDGLTTNGVLVMPRGFTTTSQPGVWREISVCGDVYLTBETSAQQRGKLVESETVNL 240  
Dy 181 HMDGLTTNGVLVMPRGFTTTSQPGVWREISVCGDVYLTBETSAQQRGKLVESETVNL 240

Qy 241 QDSSLIDIGATLWRDTADGLHTPTOKRHKIALEQINARAPCPVGLNTLAFFSINKE 300  
Dy 241 QDSSLIDIGATLWRDTADGLHTPTOKRHKIALEQINARAPCPVGLNTLAFFSINKE 300

Qy 301 VWEKQPMAYLSCHVHGTHNGRSDTEANERCPMRTVGVPLWLGCEAGFYVDAG 360  
Dy 301 VWEKQPMAYLSCHVHGTHNGRSDTEANERCPMRTVGVPLWLGCEAGFYVDAG 360

Qy 301 VWEKQPMAYLSCHVHGTHNGRSDTEANERCPMRTVGVPLWLGCEAGFYVDAG 360  
Dy 301 VWEKQPMAYLSCHVHGTHNGRSDTEANERCPMRTVGVPLWLGCEAGFYVDAG 360

Qy 361 PPTHAFTPCGHVSEKSAKWSQIPLPHGTHAFHAACPFCAOLVGEONCILIFOQPID 420  
Dy 361 PPTHAFTPCGHVSEKSAKWSQIPLPHGTHAFHAACPFCAOLVGEONCILIFOQPID 420

RESULT 3  
US-09-843-905A-8  
Sequence 8, Application US/09843905A  
Publication No. US2002016683A1  
GENERAL INFORMATION:  
APPLICANT: Cosman, David J.  
TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
FILE REFERENCE: 2990-A  
CURRENT APPLICATION NUMBER: US/09/843, 905A  
CURRENT FILING DATE: 2001-04-27  
PRIOR APPLICATION NUMBER: US 60/200.198  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-843-905A-8

Query Match 99.7%; Score 2283; DB 3; Length 420;  
Best Local Similarity 99.8%; Pred. No. 7; gape 216;  
Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFSPGQEEHCAPNKEPVKYGELVWYNGALPNCDRGRKRKFALYKRPKANGVKSTVH 60  
Dy 1 MFSPGQEEHCAPNKEPVKYGELVWYNGALPNCDRGRKRKFALYKRPKANGVKSTVH 60

Qy 61 VISTPOASKAISCKGHOHSISYTLRSNOTWVYTHDKDTDFQVGISTTESPIDEFVTTI 120  
Dy 61 VISTPOASKAISCKGHOHSISYTLRSNOTWVYTHDKDTDFQVGISTTESPIDEFVTTI 120

Qy 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYTRIFAGPSSKNFLGEAKWKPDG 180  
Dy 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYTRIFAGPSSKNFLGEAKWKPDG 180

Qy 181 HMDGLTTNGVLVMPRGFTTTSQPGVWREISVCGDVYLTBETSAQQRGKLVESETVNL 240  
Dy 181 HMDGLTTNGVLVMPRGFTTTSQPGVWREISVCGDVYLTBETSAQQRGKLVESETVNL 240

Qy 241 QDSSLIDIGATLWRDTADGLHTPTOKRHKIALEQINARAPCPVGLNTLAFFSINKE 300  
Dy 241 QDSSLIDIGATLWRDTADGLHTPTOKRHKIALEQINARAPCPVGLNTLAFFSINKE 300

Qy 301 VWEKQPMAYLSCHVHGTHNGRSDTEANERCPMRTVGVPLWLGCEAGFYVDAG 360  
Dy 301 VWEKQPMAYLSCHVHGTHNGRSDTEANERCPMRTVGVPLWLGCEAGFYVDAG 360

Qy 361 PPTHAFTPCGHVSEKSAKWSQIPLPHGTHAFHAACPFCAOLVGEONCILIFOQPID 420  
Dy 361 PPTHAFTPCGHVSEKSAKWSQIPLPHGTHAFHAACPFCAOLVGEONCILIFOQPID 420

RESULT 4  
US-10-317-250-8  
Sequence 8, Application US/10317250  
Publication No. US20030165945A1  
GENERAL INFORMATION:  
APPLICANT: Bird, Timothy A.  
APPLICANT: Cosman, David J.  
APPLICANT: Li, Xiaoxia  
TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
FILE REFERENCE: 2990-B  
CURRENT APPLICATION NUMBER: US/10/317, 250  
CURRENT FILING DATE: 2002-12-11  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 420  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-317-250-8

Query Match 99.7%; Score 2283; DB 4; Length 420;  
 Best Local Similarity 99.8%; Pred. No. 7.7e-216; Indels 0; Gaps 0;  
 Matches 419; Conservative 0; Mismatches 1;

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QY 1 MFSPGQEBHCAPKEPKVKGELVWLGNGALPNDGRKRSFALKYKPKANGVKPSTH 60
Db 1 MFSPGQEBHCAPKEPKVKGELVWLGNGALPNDGRKRSFALKYKPKANGVKPSTH 60
QY 61 VISTPOASKAISCKGQHSISYTTSRNOTVWVYTHDKDQMFGVRSTESPIDFWVTI 120
Db 61 VISTPOASKAISCKGQHSISYTTSRNOTVWVYTHDKDQMFGVRSTESPIDFWVTI 120
QY 61 VISTPOASKAISCKGQHSISYTTSRNOTVWVYTHDKDQMFGVRSTESPIDFWVTI 120
Db 61 VISTPOASKAISCKGQHSISYTTSRNOTVWVYTHDKDQMFGVRSTESPIDFWVTI 120
QY 121 SGSONTDEAQITOSTISFACTIVCDRNPYTAIFAGFDSSNIFGEKAQKWNPDG 180
Db 121 SGSONTDEAQITOSTISFACTIVCDRNPYTAIFAGFDSSNIFGEKAQKWNPDG 180
QY 181 HMDGLITTINGVLUWHRGGTEESQPGVWRRELISVGDDVTLRETRSAORGKLVESETNVL 240
Db 181 HMDGLITTINGVLUWHRGGTEESQPGVWRRELISVGDDVTLRETRSAORGKLVESETNVL 240
QY 241 QDSLSDIDCGATLWRTADGLFTPTOKHIALEQETINARPCPVGANTLAFFSINK 300
Db 241 QDSLSDIDCGATLWRTADGLFTPTOKHIALEQETINARPCPVGANTLAFFSINK 300
QY 241 QDSLSDIDCGATLWRTADGLFTPTOKHIALEQETINARPCPVGANTLAFFSINK 300
Db 241 QDSLSDIDCGATLWRTADGLFTPTOKHIALEQETINARPCPVGANTLAFFSINK 300
QY 301 VWERKOPWAVLSGHHVGHYHNGHRSDEANERCPMCTVGPVPLMGCEAGFYVDAG 360
Db 301 VWERKOPWAVLSGHHVGHYHNGHRSDEANERCPMCTVGPVPLMGCEAGFYVDAG 360
QY 361 PPTHAFTPCHVSEKSKAKYMSQIPLHGTHAFHAACPFCATOLVGEONCILKIFQPID 420
Db 361 PPTHAFTPCHVSEKSKAKYMSQIPLHGTHAFHAACPFCATOLVGEONCILKIFQPID 420
QY 361 PPTHAFTPCHVSEKSKAKYMSQIPLHGTHAFHAACPFCATOLVGEONCILKIFQPID 420
Db 361 PPTHAFTPCHVSEKSKAKYMSQIPLHGTHAFHAACPFCATOLVGEONCILKIFQPID 420

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**RESULT 5**  
 US-10-258-703-8  
 ; Sequence 8; Application US/10258703  
 ; Publication No. US2004034199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Cosman, David J.  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; FILE REFERENCE: 2990-US  
 ; CURRENT APPLICATION NUMBER: US/09/843, 905A  
 ; PRIORITY DATE: 2000-04-28  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 419  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-09-843-905A-6

Query Match 95.0%; Score 2175.5; DB 3; Length 419;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-205; Indels 1; Gaps 1;  
 Matches 399; Conservative 10; Mismatches 10;

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QY 1 MFSPGQEBHCAPKEPKVKGELVWLGNGALPNDGRKRSFALKYKPKANGVKPSTH 60
Db 1 MFSPGQEBHCAPKEPKVKGELVWLGNGALPNDGRKRSFALKYKPKANGVKPSTH 60
QY 61 VISTPOASKAISCKGQHSISYTTSRNOTVWVYTHDKDQMFGVRSTESPIDFWVTI 120
Db 61 VISTPOASKAISCKGQHSISYTTSRNOTVWVYTHDKDQMFGVRSTESPIDFWVTI 120
QY 121 SGSONTDEAQITOSTISFACTIVCDRNPYTAIFAGFDSSNIFGEKAQKWNPDG 180
Db 121 SGSONTDEAQITOSTISFACTIVCDRNPYTAIFAGFDSSNIFGEKAQKWNPDG 179
QY 181 HMDGLITTINGVLUWHRGGTEESQPGVWRRELISVGDDVTLRETRSAORGKLVESETNVL 240
Db 181 HMDGLITTINGVLUWHRGGTEESQPGVWRRELISVGDDVTLRETRSAORGKLVESETNVL 240
QY 241 QDSLSDIDCGATLWRTADGLFTPTOKHIALEQETINARPCPVGANTLAFFSINK 300
Db 241 QDSLSDIDCGATLWRTADGLFTPTOKHIALEQETINARPCPVGANTLAFFSINK 299
QY 301 VWERKOPWAVLSGHHVGHYHNGHRSDEANERCPMCTVGPVPLMGCEAGFYVDAG 360
Db 301 VWERKOPWAVLSGHHVGHYHNGHRSDEANERCPMCTVGPVPLMGCEAGFYVDAG 359
QY 361 PPTHAFTPCHVSEKSKAKYMSQIPLHGTHAFHAACPFCATOLVGEONCILKIFQPID 420
Db 361 PPTHAFTPCHVSEKSKAKYMSQIPLHGTHAFHAACPFCATOLVGEONCILKIFQPID 419

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**RESULT 7**  
 US-10-317-250-6  
 ; Sequence 6; Application US/10317250  
 ; Publication No. US20030165945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.

APPLICANT: Cozman, David J.  
 APPLICANT: Li, Xiaoxia  
 TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 FILE REFERENCE: 2990-US  
 CURRENT APPLICATION NUMBER: US/10/317,250  
 NUMBER OF SEQ ID NOS: 15  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6  
 LENGTH: 419  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-317-250-6

Query Match 95.0%; Score 2175.5; DB 4; Length 419;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-205; Mismatches 10; Indels 1; Gaps 1;  
 Matches 399; Conservative 10;

QY 1 MFSPGQEEHCAPNKEPKVYGEVLVINGALPNGDRGRKSRFLYKPKANGVKPSTH 60  
 1 MFSPGQEEPSAPNKEPKVYGEVLVINGALPNGDRGRKSRFLYKPKANGVKPSTH 60

QY 61 VISTPOQASCAISCKGQHSISYTSLRSQTVWVYTHDKDQMFGVQGSTESP1DFVVDTI 120  
 Db 61 VISTPOQASCAISCKGQHSISYTSLRSQTVWVYTHDKDQMFGVQGSTESP1DFVVDTI 120

Db 121 SGSQNTDRAQTOSTISRFACRIVCDRNEPYTARIFAGFESSKNFLGEKAQKWNPDG 180  
 QY 121 SGSQNTDRAQTOSTISRFACRIVCDRNEPYTARIFAGFESSKNFLGEKAQKWNPDG 180

QY 181 HDMLGLTTGVWMPREGFTESQPGWREISVGQDWTURTSAQQRGKLVESTINVL 240  
 Db 181 HDMLGLTTGVWMPREGFTESQPGWREISVGQDWTURTSAQQRGKLVESTINVL 240

Db 180 HDMLGLTTGVWMPREGFTESQPGWREISVGQDWTURTSAQQRGKLVESTINVL 239  
 QY 180 HDMLGLTTGVWMPREGFTESQPGWREISVGQDWTURTSAQQRGKLVESTINVL 239

QY 181 HDMLGLTTGVWMPREGFTESQPGWREISVGQDWTURTSAQQRGKLVESTINVL 240  
 Db 180 HDMLGLTTGVWMPREGFTESQPGWREISVGQDWTURTSAQQRGKLVESTINVL 239

QY 241 QDSSLIDLGATLWRTRADGLFHTPTOKHIEALRQBINARPOCPVGNTLAFFSINKE 300  
 Db 241 QDSSLIDLGATLWRTRADGLFHTPTOKHIEALRQBINARPOCPVGNTLAFFSINKE 300

QY 240 QDSSLIDLGATLWRTRADGLFHTPTOKHIEALRQBINARPOCPVGNTLAFFSINKE 299  
 Db 240 QDSSLIDLGATLWRTRADGLFHTPTOKHIEALRQBINARPOCPVGNTLAFFSINKE 299

QY 301 VVEEKOPWAYLSCHGHHVGHYHNHRSDTEANERBCPMERTGVPGVPLWLGCEAGFYVDAG 360  
 Db 301 VVEEKOPWAYLSCHGHHVGHYHNHRSDTEANERBCPMERTGVPGVPLWLGCEAGFYVDAG 359

QY 361 RPTHAFTPCGHYSEKSKYMSQIPLRGTHAFAACPCATOLVQBNONCILKLIQGPID 420  
 Db 361 RPTHAFTPCGHYSEKSKYMSQIPLRGTHAFAACPCATOLVQBNONCILKLIQGPID 419

Db 360 RPTHAFTPCGHVSEKSKYMSQIPLRGTHAFAACPCATOLVQBNONCILKLIQGPID 419

RESULT 8

US-10-258-703-6

; Sequence 6, Application US/10258703  
 ; Publication No. US20040034199A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; APPLICANT: Cozman, David J.  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; FILE REFERENCE: 2990-US  
 ; CURRENT APPLICATION NUMBER: US/10/258,703  
 ; CURRENT FILING DATE: 2002-10-24  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 6  
 ; LENGTH: 419  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus

Query Match 99.0%; Score 2175.5; DB 4; Length 419;  
 Best Local Similarity 95.0%; Pred. No. 3.1e-205; Mismatches 10; Indels 1; Gaps 1;  
 Matches 399; Conservative 10;

QY 1 MFSPGQEEHCAPNKEPKVYGEVLVINGALPNGDRGRKSRFLYKPKANGVKPSTH 60  
 1 MFSPGQEEPSAPNKEPKVYGEVLVINGALPNGDRGRKSRFLYKPKANGVKPSTH 60

QY 61 VISTPOQASCAISCKGQHSISYTSLRSQTVWVYTHDKDQMFGVQGSTESP1DFVVDTI 120  
 Db 61 VISTPOQASCAISCKGQHSISYTSLRSQTVWVYTHDKDQMFGVQGSTESP1DFVVDTI 120

QY 61 MFSPGQEEPSAPNKEPKVYGEVLVINGALPNGDRGRKSRFLYKPKANGVKPSTH 60  
 1 MFSPGQEEPSAPNKEPKVYGEVLVINGALPNGDRGRKSRFLYKPKANGVKPSTH 60

QY 121 SGSQNTDRAQTOSTISRFACRIVCDRNEPYTARIFAGFESSKNFLGEKAQKWNPDG 179  
 Db 121 SGSQNTDRAQTOSTISRFACRIVCDRNEPYTARIFAGFESSKNFLGEKAQKWNPDG 179

RESULT 10  
 US-09-843-905A-4  
 ; Sequence 4, Application US/09843905A  
 ; Patent No. US2002165683A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; INVENTOR: Cosman, David J.  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; FILE REFERENCE: 2990-A  
 ; CURRENT APPLICATION NUMBER: US/10/317,250  
 ; CURRENT FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 418  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-843-905A-4

RESULT 10

US-09-843-905A-4

; Sequence 4, Application US/09843905A

; Patent No. US2002165683A1

; GENERAL INFORMATION:

; APPLICANT: Bird, Timothy A.

; INVENTOR: Cosman, David J.

; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES

; FILE REFERENCE: 2990-A

; CURRENT APPLICATION NUMBER: US/10/317,250

; CURRENT FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-843-905A-4

Query Match 83.7%; Score 1917; DB 3; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-843-905A-4

RESULT 11  
 US-10-317-250-4  
 ; Sequence 4, Application US/10317250  
 ; Publication No. US20030165945A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bird, Timothy A.  
 ; INVENTOR: Li, Xiaoxia  
 ; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
 ; FILE REFERENCE: 2990-B  
 ; CURRENT APPLICATION NUMBER: US/10/317,250  
 ; CURRENT FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 4  
 ; LENGTH: 418  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-317-250-4

RESULT 11

US-10-317-250-4

; Sequence 4, Application US/10317250

; Publication No. US20030165945A1

; GENERAL INFORMATION:

; APPLICANT: Bird, Timothy A.

; INVENTOR: Li, Xiaoxia

; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES

; FILE REFERENCE: 2990-B

; CURRENT APPLICATION NUMBER: US/10/317,250

; CURRENT FILING DATE: 2002-12-11

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

Query Match 83.7%; Score 1917; DB 4; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 9.4e-180; Indels 2; Gaps 1;  
 Matches 342; Conservative 38; Mismatches 38; Insertions 2; Gaps 1;

; CURRENT FILING DATE: 2001-04-27

; PRIOR APPLICATION NUMBER: US 60/200,198

; PRIOR FILING DATE: 2000-04-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-317-250-4

; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-443-108-10

Query Match      83.7%; Score 1917; DB 4; Length 418;  
Best Local Similarity 81.4%; Pred. No. 9.4e-180; Mismatches 38; Indels 2; Gaps 1;  
Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;

QY 1 MPSQGEEHCAPIKEPVKGELVGLGNGALPNSDRGRKSRFLYKPKANGVKPSTH 60  
Db 1 MFSPOENH--PSKAPVKVKGELVGLGNGALPNSDRGRKSRFLYKPKANGVKPSTH 58

QY 61 VISTPQASKAISCKQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 120  
Db 59 IACTPOAKAISNKDQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 118

QY 121 SGSONTDEAQITOSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 180  
Db 119 PGSOQNSTDQSQVSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 178

QY 121 SGSONTDEAQITOSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 83.7%; Score 1917; DB 4; Length 418;  
Pred. No. 9.4e-180; Mismatches 38; Indels 2; Gaps 1;  
Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;

QY 61 VISTPQASKAISCKQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 120  
Db 59 IACTPOAKAISNKDQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 118

QY 121 SGSONTDEAQITOSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 83.7%; Score 1913; DB 4; Length 418;  
Pred. No. 2.3e-179; Mismatches 37; Indels 2; Gaps 1;  
Matches 342; Conservative 37; Mismatches 39; Indels 2; Gaps 1;

QY 61 VISTPQASKAISCKQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 120  
Db 59 IACTPOAKAISNKDQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 118

QY 181 HMDGLITTMGVUWMPRGFTESQPGWRETSVCGVYTLBTRSAQRCGLVSEETNL 240  
Db 179 QMDGLITTMGVUWMPRGFTESQPGWRETSVCGVYTLBTRSAQRCGLVSEETNL 238

QY 241 QDSLIDICATILWRADGLFHTPTKHEALRQEINARQPCPGNTLAPSINRE 300  
Db 239 QDSLIDICATILWRADGLFHTPTKHEALRQEINARQPCPGNTLAPSINRE 298

QY 301 VVERKQPAYLSCGHVHGYNHNGRSDEANRECPCMCRTVCPYVPLWLGCEAGFYVDAG 360  
Db 239 VDEKQPWYLNCGHVHGYNHNGRSDEANRECPCMCRTVCPYVPLWLGCEAGFYVDAG 358

QY 361 PPTHAFTCGHCESEKSKYWSQIPLPGHTFAHACPCATOLVGBONCIKLIFGPD 420  
Db 359 PPTHAFTCGHCESEKSKYWSQIPLPGHTFAHACPCATOLVGBONCIKLIFGPD 418

RESULT 14  
US-10-041-030-2  
; Sequence 2, Application US/10041030  
; Publication No. US20020150934A1  
; GENERAL INFORMATION:  
; APPLICANT: Powers, Scott  
; APPLICANT: Mu, David  
; APPLICANT: Xiang, Phil  
; APPLICANT: Peng, Yue  
; APPLICANT: Tularik Inc.  
; TITLE OF INVENTION: Diagnosis and Treatment of Cancer Using Mammalian  
; TITLE OF INVENTION: Pellino Polypeptides and Polynucleotides  
; FILE REFERENCE: 01781-006810US  
; CURRENT APPLICATION NUMBER: US/10/041,030  
; CURRENT FILING DATE: 2001-12-28  
; PRIOR APPLICATION NUMBER: US 60/259,502  
; PRIOR FILING DATE: 2001-01-02  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human pellino 1  
; US-10-041-030-2

Query Match      83.5%; Score 1913; DB 4; Length 418;  
Best Local Similarity 81.4%; Pred. No. 2.3e-179; Mismatches 37; Indels 2; Gaps 1;  
Matches 342; Conservative 37; Mismatches 39; Indels 2; Gaps 1;

QY 1 MPSQGEEHCAPIKEPVKGELVGLGNGALPNSDRGRKSRFLYKPKANGVKPSTH 60  
Db 1 MFSPOENH--PSKAPVKVKGELVGLGNGALPNSDRGRKSRFLYKPKANGVKPSTH 58

QY 61 VISTPQASKAISCKQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 120  
Db 59 IACTPOAKAISNKDQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 118

QY 121 SGSONTDEAQITOSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 180  
Db 119 PGSOQNSTDQSQVSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 178

QY 181 HMDGLITTMGVUWMPRGFTESQPGWRETSVCGVYTLBTRSAQRCGLVSEETNL 240  
Db 179 QMDGLITTMGVUWMPRGFTESQPGWRETSVCGVYTLBTRSAQRCGLVSEETNL 238

QY 241 QDSLIDICATILWRADGLFHTPTKHEALRQEINARQPCPGNTLAPSINRE 300  
Db 239 QDSLIDICATILWRADGLFHTPTKHEALRQEINARQPCPGNTLAPSINRE 298

QY 301 VVERKQPAYLSCGHVHGYNHNGRSDEANRECPCMCRTVCPYVPLWLGCEAGFYVDAG 360  
Db 239 VDEKQPWYLNCGHVHGYNHNGRSDEANRECPCMCRTVCPYVPLWLGCEAGFYVDAG 358

QY 361 PPTHAFTCGHCESEKSKYWSQIPLPGHTFAHACPCATOLVGBONCIKLIFGPD 420  
Db 359 PPTHAFTCGHCESEKSKYWSQIPLPGHTFAHACPCATOLVGBONCIKLIFGPD 418

RESULT 13  
US-10-258-703-4  
; Sequence 4, Application US/10258703  
; Publication No. US2004003199A1  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Cozman, David J.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-US  
; CURRENT APPLICATION NUMBER: US/10/258,703  
; CURRENT FILING DATE: 2002-10-24  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: human pellino 1  
; US-10-041-030-2

Query Match      83.7%; Score 1917; DB 4; Length 418;  
Best Local Similarity 81.4%; Pred. No. 9.4e-180; Mismatches 38; Indels 2; Gaps 1;  
Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;

QY 1 MPSQGEEHCAPIKEPVKGELVGLGNGALPNSDRGRKSRFLYKPKANGVKPSTH 60  
Db 1 MFSPOENH--PSKAPVKVKGELVGLGNGALPNSDRGRKSRFLYKPKANGVKPSTH 58

QY 61 VISTPQASKAISCKQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 120  
Db 59 IACTPOAKAISNKDQHSISYTLSRNQTVWVYTHDKDQDMFQGRSTESPIDFWTTI 118

QY 121 SGSONTDEAQITOSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 180  
Db 119 PGSOQNSTDQSQVSTISRFACTRCRDRNPRYTAIFAGFDSSKNIPGKAKWKNDG 178

QY 181 HMDGLITTMGVUWMPRGFTESQPGWRETSVCGVYTLBTRSAQRCGLVSEETNL 240  
Db 179 QMDGLITTMGVUWMPRGFTESQPGWRETSVCGVYTLBTRSAQRCGLVSEETNL 238

QY 241 QDSLIDICATILWRADGLFHTPTKHEALRQEINARQPCPGNTLAPSINRE 300  
Db 239 QDSLIDICATILWRADGLFHTPTKHEALRQEINARQPCPGNTLAPSINRE 298

QY 301 VVERKQPAYLSCGHVHGYNHNGRSDEANRECPCMCRTVCPYVPLWLGCEAGFYVDAG 360  
Db 239 VDEKQPWYLNCGHVHGYNHNGRSDEANRECPCMCRTVCPYVPLWLGCEAGFYVDAG 358

QY 361 PPTHAFTCGHCESEKSKYWSQIPLPGHTFAHACPCATOLVGBONCIKLIFGPD 420  
Db 359 PPTHAFTCGHCESEKSKYWSQIPLPGHTFAHACPCATOLVGBONCIKLIFGPD 418

Search completed: March 1, 2006, 21:04:32  
Job time : 168 secs

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OM protein - protein search, using sw model  
Run on: March 1, 2006, 21:00:16 ; Search time 47 seconds  
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ALIGNMENT

US-09-843-905A-8  
; Sequence 8, Application US/09843905A  
; Patent No. 6703487  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Comman, David J.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-A  
; CURRENT APPLICATION NUMBER: US109/843,905A  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60\_200\_198  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 420  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-843-905A-8

Sequence 32215, Ap  
Sequence 10252, A  
Sequence 32, Appl  
Sequence 3891, Ap  
Sequence 1905, A  
Sequence 16024, A  
Sequence 7599, Ap  
Sequence 7600, Ad  
Patent No. 5455158  
Sequence 235, App  
Sequence 12, Appl  
Sequence 1, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 4, Appl  
Sequence 3, Appl  
Sequence 6, Appl  
Sequence 9771, Ap

Db 361 PPTHAFTPCGHVCSEKSAKWSQIPLPHGTHAFRACPFATOLVGEONCILKLFQGPID 420 ; SEQ ID NO 4 ; LENGTH: 418 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-843-905A-4

RESULT 2

; Sequence 6, Application US/09843905A  
; Patent No. 6703487  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-A  
; CURRENT APPLICATION NUMBER: US/09/843, 905A  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,198  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 419  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-843-905A-6

Query Match 83.7%; Score 1917; DB 2; Length 418;  
Best Local Similarity 81.4%; Pred. No. 3.1e-198;  
Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;

Qy 1 MFSPGQEBHCAPKKEPKYKELVULGNGALPNDGRGRKSRPALYKRPKANGVKSTVH 60  
Do 1 MFSPDQENH--PSKAPYKTYKELVULGNGALPNDGRGRKSRPALYKRPKANGVKSTVH 58  
Qy 61 VISTPOASKAISCKGQHSISYLSRNOTVVWVYTHDKDMDQVGSTESPIDFVWMTD 120  
Do 59 IACTPOASKAISCKGQHSISYLSRNOTVVWVYTHDSNDMFOIGRSTESPIDFVWMTD 118

Qy 121 SESQNTDAQITQTSRFACTIVCDNEPYTARIAGPFOSSKNIFLGEKAAKWKNPDG 180  
Do 119 PSQSQNSDTSQSYOSTISRFACRICKERNPFTARYAGFDSSKNIFLGEKAAKWKNSDG 178

Qy 181 HMDGLLTGVNLWHPRGFTERSOPGVWREISVCGDVYTRETRSAQORGKLVESETNVL 240  
Do 179 QMDGLLTGVNLWHPRGFTERSKPGVWREISVCGDVWFLRTSQAORGKLVETNQL 238

Qy 241 QDSSLIDICGATLWRTDGLFHTPTOKTEALROEINARPOCPVGLNTLAFFSPINRK 300  
Do 239 QDSSLIDICGATLWRTDGLFHTPTOKTEALROEINARPOCPVGLNTLAFFSPINRKD 298

Qy 301 VWERKQPAVYLSCGHVHGHHNGHSDETEAMERECNCRTYGPVPLWLGEAGFYVDAG 360  
Do 299 VDEKQPVWLYNGHVGHHNGKKEERDGKORECPMCRSVGPVPLWLGEAGFYVDAG 358

Qy 361 PPTHAFTPCGHVCSEKSAKWSQIPLPHGTHAFRACPFATOLVGEONCILKLFQGPID 420  
Do 359 PPTHAFTPCGHVCSEKSAKWSQIPLPHGTHAFRACPFATOLVGEONCILKLFQGPID 418

RESULT 4

; Sequence 2, Application US/09843905A  
; Patent No. 6703487  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-A  
; CURRENT APPLICATION NUMBER: US/09/843, 905A  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,198  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 418  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-843-905A-2

Query Match 83.5%; Score 1912; DB 2; Length 418;  
Best Local Similarity 81.2%; Pred. No. 1.1e-197;  
Matches 341; Conservative 39; Mismatches 38; Indels 2; Gaps 1;

Qy 1 MFSPGQEBHCAPKKEPKYKELVULGNGALPNDGRGRKSRPALYKRPKANGVKSTVH 60  
Do 1 MFSPDQENH--PSKAPYKTYKELVULGNGALPNDGRGRKSRPALYKRPKANGVKSTVH 58  
Qy 61 VISTPOASKAISCKGQHSISYLSRNOTVVWVYTHDKDMDQVGSTESPIDFVWMTD 120  
Do 59 IACTPOASKAISCKGQHSISYLSRNOTVVWVYTHDSNDMFOIGRSTESPIDFVWMTD 118

Qy 121 SESQNTDAQITQTSRFACTIVCDNEPYTARIAGPFOSSKNIFLGEKAAKWKNPDG 180

RESULT 5  
US-09-843-905A-12  
; Sequence 12, Application US/09843905A  
; Patient No. 670487  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-A  
; CURRENT APPLICATION NUMBER: US/09/843, 905A  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,198  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-843-905A-12

Query Match 71.7%; Score 1642; DB 2; Length 445;  
Best Local Similarity 71.4%; Pred. No. 2e-168;  
Matches 299; Conservative 42; Mismatches 74; Indels 4; Gaps 3;

QY 3 SPGOBERHCAPNKERVVKYGVSLVULGYNGALPNGDRGRRSRFLAJXKRKPRAANGVPRSTVNU 62  
Db 30 SPG--EDAQGEPIKYLE-----I 48

QY 63 STPOASKASLCKQHSISSTSYLSRNQTVTEYHDKDIMPWRSTSSRIDVTDTSG 122  
Db 49 STPLVSKLNSRGHQSISSTYLSRSHSVIVEYHTSDATMDFOLGRSTMIDFVUTDASPQ 108

QY 123 SQTDEAQITQTSRFACTIVCDRNPEPYTARIAAGFDSSNIFLGKAQKWNPDGHM 182  
Db 109 G-GRAEGISAQSTSRKICLDRPFYTAIYAAGFDASSNIFLGRAKWRTPGM 167

QY 183 DGLITNGVLMHPRGGFEESPGWBRBISVGDDVYLTRETSQAQGKLVSEETNTQD 242  
Db 168 DGLITNGVLMHPRGGFEESPGWBRBISVGDDVYLTRETSQAQGKLVSEETNTQD 227

QY 243 GSLIDCATLWRTADLFLPKTOKIEAROEINAARPOCVGTLTAFPSINRKV 302  
Db 228 GSLIDCATLWRTADLFLPKTOKIEAROEINAARPOCVGTLTAFPSARRTA 287

QY 303 EEK-OPWAVLSCHVHGHNWGRSDTANERBZCPMCRTVGVYVPLMGCEAGFYVDGP 361  
Db 288 DPKQWPWTVRCGVHGHNWGRSDTANERBZCPMCRTVGVYVPLMGCEAGFYVDGP 347

QY 352 PTAFTPGHVESEKSAKWSQPLPHGTHAAACPCFCATOLVGEONCILIFQGPID 420  
Db 348 PSHPAPCGHVCEKTYWAQPLPHGTHAAACPCFCAGMLTGEGHGCVRUHQGPID 406

QY 123 SQTDEAQITQTSRFACTIVCDRNPEPYTARIAAGFDSSNIFLGKAQKWNPDGHM 182  
Db 148 G-GRAEGISAQSTSRKICLDRPFYTAIYAAGFDASSNIFLGRAKWRTPGM 206

QY 183 DGLITNGVLMHPRGGFEESPGWBRBISVGDDVYLTRETSQAQGKLVSEETNTQD 242  
Db 207 GLITNGVLMHPRGGFEESPGWBRBISVGDDVYLTRETSQAQGKLVSEETNTQD 266

QY 243 GSLIDCATLWRTADLFLPKTOKIEAROEINAARPOCVGTLTAFPSINRKV 302  
Db 267 GSLIDCATLWRTADLFLPKTOKIEAROEINAARPOCVGTLTAFPSINRKV 326

QY 303 EK-OPWAVLSCHVHGHNWGRSDTANERBZCPMCRTVGVYVPLMGCEAGFYVDGP 361  
Db 327 PKQWPWTVRCGVHGHNWGRSDTANERBZCPMCRTVGVYVPLMGCEAGFYVDGP 386

QY 362 PTAFTPGHVESEKSAKWSQPLPHGTHAAACPCFCATOLVGEONCILIFQGPID 420  
Db 387 PSHPAPCGHVCEKTYWAQPLPHGTHAAACPCFCAGMLTGEGHGCVRUHQGPID 445

RESULT 6  
US-10-104-047-3928  
; Sequence 3928, Application US/10104047  
; Patient No. 694241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. 694241el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104, 047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3928  
; LENGTH: 406  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-104-047-3928

Query Match 64.7%; Score 1482.5; DB 2; Length 406;  
Best Local Similarity 65.6%; Pred. No. 3e-151;  
Matches 275; Conservative 36; Mismatches 65; Indels 43; Gaps 4;

QY 3 SPGOBERHCAPNKERVVKYGVSLVULGYNGALPNGDRGRRSRFLAJXKRKPRAANGVPRSTVNU 62  
Db 30 SPG--EDAQGEPIKYLE-----I 48

QY 63 STPOASKASLCKQHSISSTSYLSRNQTVTEYHDKDIMPWRSTSSRIDVTDTSG 122  
Db 49 STPLVSKLNSRGHQSISSTYLSRSHSVIVEYHTSDATMDFOLGRSTMIDFVUTDASPQ 108

QY 123 SQTDEAQITQTSRFACTIVCDRNPEPYTARIAAGFDSSNIFLGKAQKWNPDGHM 182  
Db 109 G-GRAEGISAQSTSRKICLDRPFYTAIYAAGFDASSNIFLGRAKWRTPGM 167

QY 183 DGLITNGVLMHPRGGFEESPGWBRBISVGDDVYLTRETSQAQGKLVSEETNTQD 242  
Db 168 DGLITNGVLMHPRGGFEESPGWBRBISVGDDVYLTRETSQAQGKLVSEETNTQD 227

QY 243 GSLIDCATLWRTADLFLPKTOKIEAROEINAARPOCVGTLTAFPSINRKV 302  
Db 228 GSLIDCATLWRTADLFLPKTOKIEAROEINAARPOCVGTLTAFPSARRTA 287

QY 303 EEK-OPWAVLSCHVHGHNWGRSDTANERBZCPMCRTVGVYVPLMGCEAGFYVDGP 361  
Db 288 DPKQWPWTVRCGVHGHNWGRSDTANERBZCPMCRTVGVYVPLMGCEAGFYVDGP 347

QY 352 PTAFTPGHVESEKSAKWSQPLPHGTHAAACPCFCATOLVGEONCILIFQGPID 420  
Db 348 PSHPAPCGHVCEKTYWAQPLPHGTHAAACPCFCAGMLTGEGHGCVRUHQGPID 406

RESULT 7  
US-09-843-905A-13  
; Sequence 13, Application US/09843905A  
; Patient No. 670487  
; GENERAL INFORMATION:  
; APPLICANT: Bird, Timothy A.  
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES  
; FILE REFERENCE: 2990-A  
; CURRENT APPLICATION NUMBER: US/09/843, 905A  
; CURRENT FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/200,198  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 424  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster



RESULT 10  
 US-09-252-991A-25700  
 ; Sequence 25700, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; NUMBER OR SEQUENCE: PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME  
 ; NUMBER OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 624 Ninth Street, N.W., Suite 300  
 ; CITY: Washington

US-09-252-991A-25700  
 ; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: *Pseudomonas aeruginosa*

Query Match 4.5%; Score 104; DB 2; Length 710;  
 Best Local Similarity 22.3%; Pred. No. 0.1;  
 Matches 90; Conservative 44; Mismatches 162; Indels 108; Gaps 21;

Qy 29 |GALENGDRGRKSERFALYKRKKANGVKUSTVHISTPOASKATS-----CKGQ 76  
 Db 264 GlQdAARRRARRAVIGR-RARRGARPRTRIVESTPMSANSELTDIAVGGAGI 322  
 Qy 77 HSTSYTSLRSNOTVWVBYTHDKDITDMQFGRSTSPIDFWVTPTSGSNTDQAQTOSTI 136  
 Db 323 GVIASLLRKSPGKRLSPLEPADTHYQPCWTLVGGAYAQGDTA----RPMGLVPPGV 377

Qy 137 SRFACRIVCDRNENYTAIRFAAGDS--SKNIFL--GEKAOKWQPDHMDGSDITTCV-- 190  
 Db 378 EMLRTRV--ERVPDEARRLLEEDSLEYRNLTVCPGLRA-WERIEGLBETLGRRNGVTS 434  
 Qy 191 -----LYMHPROG--FTESOPGVMREISVCGDVLTRETRSAORGKLVES 235  
 Db 435 NYXVDLAPTYWEVJRGKGALKFTQAMP---IKCAG---APOKAMISC 479  
 Qy 236 E---TNYLQDGSL--IDLGATIWLWTADGLHEPTKHTQHIELRQETNAARIQCPVGINT 290  
 Db 480 DHMIREGVLIQDIEVEFDLAGA-LFGVQAD--FVPLIMEVRKYSSEL----AFNSNL 529

Qy 291 LAPSINKKEVVEKOPWAIALSCHVHXRHMSDTEAN---ERCPMCRTVGPVIP 346  
 Db 530 VKYTGAAKKA-----WPEVKADGNNTLAEKOFDGLWVPPQLP 568

Qy 347 -----LWLGCCAGF-YVDAAGPPTA---FTP CGHVESEKSAK 379  
 Db 569 PTFVVAASGIGDAGNCCEVDPATLWVRIEGLFALGDVGCTANAK 612

RESULT 11  
 US-09-077-038A-6  
 ; Sequence 6, Application US/09077098A  
 ; General Information:  
 ; Applicant: TOKUNAGA, Eiji  
 ; SAKAGUCHI, Masashi  
 ; MATSUO, Kazuo  
 ; HAMADA, Fukasaburo  
 ; TOKIYOSHI, Sachio  
 ; Title of Invention: NOVEL POLYPEPTIDE FROM HAEMOPHILUS  
 ; Number or Sequence: PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME  
 ; Correspondence Address:  
 ; Addressee: BROWDY AND NEIMARK  
 ; Street: 624 Ninth Street, N.W., Suite 300  
 ; City: Washington

STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20001  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/077,098A  
 FILING DATE: 19-May-1998  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP97/03222  
 FILING DATE: 12-SEP-1997  
 PRIORITY NUMBER: JP 27,148/1996  
 FILING DATE: 19-SEP-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOBRAU, Anne M.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: TOKUNAGA=1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2042 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 US-09-077-038A-6

Query Match 4.4%; Score 100; DB 2; Length 2042;  
 Best Local Similarity 22.7%; Pred. No. 1.6;  
 Matches 73; Conservative 45; Mismatches 124; Indels 80; Gaps 18;

Qy 53 GVKPSTVHVISTP---QASKATSCKGOMIS---YTTSRNOTWVVEETHDKD-TDMQVY 105  
 Db 1346 GIUDTRINKKNNPADDQBNLNSUSBSGNKNAITGLWDVVKTKNSPITVSPSTDNSKKKTFVG 1405  
 Qy 106 RSTESPDPDVTTISSQNTBEAQTS-----TISFRACRIVCD-----R 147  
 Db 1406 -----VDP--TDTITGDDATDKKLTSKSVSYVNKLNPSTDILSDCRSGNATA 1457  
 Qy 148 NEPYTARTFAAGD-SSRNIFIQEK-----AAKKWNPDG-----HMDGTTN-GV 190  
 Db 1458 NDGVKRNLSDFTIKSENFTSKQKNSDSLGVMDQVFKPLSLMTLTSIANT 1517  
 Qy 191 LVWHPRGSEFTTSSQCPWVREISVCGDVTLRETRSAQRGKLVESFTNVL---PDGS- 244  
 Db 1518 FAKLUDASNLDDSNKEKWR---TALNVYSKTEVDAEIQSKVLTDFGLPATKOKSG 1574  
 Qy 245 ---LIDGATIWLWTADGLFIFT-----OKHIALRQEINARPPCFV 287  
 Db 1575 NNAGID-AGNKKISNVADGDI-SPTSCDWVTCRQLYALMQKGSRVYVGDEVSPTKPTAP 1632  
 Qy 288 LNTLAFPSINRKEVVEKQPWA 309  
 Db 1633 TN-AnPfATAPTASSQWA 1652

RESULT 12  
 US-10-192-844-6  
 ; Sequence 6, Application US/10192564  
 ; General Information:  
 ; Patent No. 693080  
 ; General Information:  
 ; Applicant: TOKUNAGA, Eiji  
 ; SAKAGUCHI, Masashi  
 ; MATSUO, Kazuo  
 ; HAMADA, Fukasaburo  
 ; TOKIYOSHI, Sachio  
 ; Title of Invention: NOVEL POLYPEPTIDE FROM HAEMOPHILUS

## PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADRESSE: BROWDY AND NEIMARK

STREET: 624 Ninth Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20001

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/192,584

FILING DATE: 11-JUL-2002

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/09/077,098

FILING DATE: 19-MAY-1998

APPLICATION NUMBER: PCT/JP97/03222

FILING DATE: 12-SEP-1997

APPLICATION NUMBER: JP 27,148/1996

FILING DATE: 19-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: KORNBAU, Anne M.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TOKUNAGA=1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 2042 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-192-584-6

## Query Match

Best Local Similarity 22.7%; Pred. No. 1.6; DB 2; Length 2042;

Matches 73; Conservative 45; Mismatches 124; Indels 80; Gaps 18;

Qy 53 GAKPSTVAVISTP--QASKASICKGHSR---YTLSRNQTWVEYHDK-TDMQVG 105

Db 1346 GLDDDTLNKINPNDQDLSNLSEKGNAATGLVUDWKTKNSPRTVERSTDNSCKTPV 1405

Qy 106 RSTESPIDRVVTISGSONTDEAQITOS----TISRPAFRIVCD----R 147

Db 1406 -----VDF-TDPRTEGATDDEKKLTTSKSVESYVTKLNSTDILSDRSGNATA 1457

Qy 148 NEPYTARTFAAGFD-SSKNIFLGSKR-----AAKWNKPDG-----HMDGTTN--GV 190

Db 1458 NDGVGKRRLSDGFTIKSENFTLGSKQYNGSDSLGVMYDQNGVFKLSLAMLTSLANT 1517

Qy 191 LVMHPRGGSTEQPGVWRREISVGDDVYTLETRRSAQORGKLVESERTVNL---QPGS- 244

Db 1518 PAKLDASNLTDISKKEKRR---TALNVVSKTEDAEOKSKVNTLPDQGLIRAKTQKG 1574

Qy 245 --LIDLCGATLLMTADQGLPHT-----QKHEALRQEINARPQCPVG 287

Db 1575 NNAGID-AGNKISNVADGDI-SPTSGDVVTGRQLYALMQKGIRVYGDVSPTKTQTTAP 1632

Qy 288 LNTLAFPSINRKEYVEEKOPWA 309

Db 1633 TN--ANPTTATPASSTQWA 1652

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CI001307

CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT FILING DATE: 2000-04-14

PRIORITY APPLICATION NUMBER: 60/241, 755

PRIORITY FILING DATE: 2000-10-20

PRIORITY APPLICATION NUMBER: 60/237, 768

PRIORITY FILING DATE: 2000-10-03

PRIORITY FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 6500

TYPE: PRT

ORGANISM: Human

US-09-949-016-6500

Query Match Best Local Similarity 4.2%; Score 96; DB 2; Length 717; Matches 71; Conservative 44; Mismatches 110; Indels 92; Gaps 16;

Qy 52 NGVKPSTHVISTPQASKAISCG-----KGKHSISYTLSRNQTVVVEYTHDKDTDMQVG 105

Db 211 DSVTNTLHLVIGGFFDAVTCIAFSKSNGGNLCAVDSDNDHVLSVWDWQEEKLADVK 270

Qy 106 RSTESPIDRVVTISGSONTDEAQITOS----TISRPAFRIVCD----SRPACRIVC---D 146

Db 271 CSNEAVFAADFHPDTDTIIVTGCTTSLLDPLRKLPLRSKDSYTRKAKVVLQVTFSE 330

Qy 147 RMEPYTAKTAFAAGPDSSKNNIF--GEKAALKWKNPDGHMDGT----TNGULVMPRG 198

Db 331 NEDTITG-----DSSGNILVWKGTPNTRISAVQGAHEGGISPLCMRQTLV--SGG 380

Qy 199 FPTBESQPGVWRRIISVCDVYLTRETRSAQQRGL--VESETNVIQDGLSLIDCGAT-- 252

Db 381 GKDR-----KLIWSGNYQKLKRKTPPEQFGPIRTVAEGKGDV-----LIGTRNF 427

Qy 253 LIWRTAQCLERHPPTQKTEAL--RQEINARPOCPVGLNTLAFFSINRKEVWEEKQWYL 311

Db 428 VLOGTLSGDFPITQGHTDELWGLATHASKPQ-----FL 461

Qy 312 SCCHVHGHNW--GHR 325

Db 462 TQCHDKHATLWDAVGR 478

RESULT 14

US-09-198-452A-485

; Sequence: 09138452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffis, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198, 452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO: 485

; LENGTH: 492

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; US-09-198-452A-485

Query Match Best Local Similarity 4.2%; Score 95.5; DB 2; Length 492;

Matches 47; Conservative 25; Mismatches 74; Indels 67; Gaps 9;

RESULT 13

US-09-949-016-6500

; Sequence 6500, Application US/0949016

QY 102 FOYGRSTESPIDRVUTPDTISGONTDEAQITOSTTISRFACTIVCDRNE----- 149  
Db 287 FTIGKLAFLDPFFSLKRDFTSYASVNAKGKVT-----LTGALVLDEHDVTDLYDMVLSQS 340  
QY 150 PYTARIFAGROSSKNIEGEAKWKGNDPGMDLTING-----VLMERPRG 197  
Db 341 PVAIPI-----AVFKGATVTKGFPDGIAATPSHYGCKWSVTSRPLIPADG 391  
QY 198 GFTFEEESQP-----GVWRBISVGCDVYTIRETSQAQRGKLYSE-----TNVL 240  
Db 392 GFGGGPSISANTLYAVWSDTJRTSTYL---DPERYGETVNSLNISPLNOAFSDIL 447  
QY 241 QDSGLIDICGATLWRTADGL---FRPTOKH 269  
Db 448 QDVLLIDHPGLSI---TAKALGAYVETPROGH 477

RESULT 15 !

US-10-197-220-65

; Sequence 65, Application US/10197220

; Patent No. 6919187

; GENERAL INFORMATION:

; APPLICANT: Gaderian, Jeff

; APPLICANT: Sibiky, Yasir A. W.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT

; TITLE OF INVENTION: AND DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121-515C3

; CURRENT APPLICATION NUMBER: US/10/197, 220

; CURRENT FILING DATE: 2002-07-15

; NUMBER OF SEQ ID NOS: 175

; SEQ ID NO 65

; LENGTH: 978

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

; US-10-197-220-65

Query Match ; 4.2%; Score 95.5; DB 2; Length 978;  
Best Local Similarity 22.1%; Pred. No. 14; Mismatches 74; Indels 67; Gaps 9;  
Matches 47; Conservative 25; Mismatches 74; Indels 67; Gaps 9;

QY 102 FOYGRSTESPIDRVUTPDTISGONTDEAQITOSTTISRFACTIVCDRNE----- 149  
Db 523 FTIGKLAFLDPFFSLKRDFTSYASVNAKGKVT-----LTGALVLDEHDVTDLYDMVLSQS 576  
QY 150 PYTARIFAGROSSKNIEGEAKWKGNDPGMDLTING-----VLMERPRG 197  
Db 577 PVAIPI-----AVFKGATVTKGFPDGIAATPSHYGCKWSVTSRPLIPADG 627  
QY 198 GFTFEEESQP-----GVWRBISVGCDVYTIRETSQAQRGKLYSE-----TNVL 240  
Db 628 GFGGGPSISANTLYAVWSDTJRTSTYL---DPERYGETVNSLNISPLNOAFSDIL 683  
QY 241 QDSGLIDICGATLWRTADGL---FRPTOKH 269  
Db 684 QDVLLIDHPGLSI---TAKALGAYVETPROGH 713

Search completed: March 1, 2006, 21:01:40  
Job time : 49 secs

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GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

### On protein - protein search, using sw model

Run on:

March 1, 2006, 20:53:05 : Search time 232 Seconds  
 (without alignments)  
 1277.250 Million cell updates/sec

Title: US-10-041-030-4

perfect score: 2290

Sequence: 1 MFSRQQEERHCAPNPKVKG.....ATOLVGEONCILKLFQGPID 420

Scoring table:

BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched:  
 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt-05\_80;\*  
 1: uniprot\_sprot;\*  
 2: uniprot\_trembl;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No.	Score	Query	Match Length	DB ID
------------	-------	-------	--------------	-------

### Description

Result No.	Score	Query	Match Length	DB ID	Description
1	2290	100.0	420	1	PELI2_HUMAN
2	2172.5	94.9	419	1	PELI2_MOUSE
3	2138.5	93.4	419	2	Q6G57_XENLA
4	2129.5	93.4	419	2	Q6P47_XENTR
5	2006	87.6	428	2	Q6DHA8_BRARE
6	1917	83.7	418	1	PELI1_HUMAN
7	1917	83.7	418	2	Q3T26_HUMAN
8	1912	83.5	418	1	PELI1_MOUSE
9	1912	83.5	418	2	Q5SRW7_MOUSE
10	1884	82.3	418	2	Q7ZKU3_XENLA
11	1864	81.4	405	2	Q5ZKU7_CHICK
12	1788	78.1	428	2	Q4SGC9_TEING
13	1647	71.9	440	2	Q4SBZ1_TEING
14	1632	71.3	445	1	PELI3_MOUSE
15	1620	70.7	469	1	PELI3_HUMAN
16	1493	65.5	400	2	Q4SGC7_TEING
17	1302	56.9	424	1	PELI1_DROME
18	1279.5	55.9	389	2	Q7RPO0_ANOGA
19	1235	53.9	455	2	Q9NDQ9_CLOIN
20	1100	48.0	441	2	Q4RLZ6_TEING
21	910	39.7	458	2	Q2657_CABEL
22	903	39.7	458	2	Q9NAE3_CABEL
23	883.5	38.6	450	2	Q6IKQ0_CABER
24	602	121	2	Q7FQm9_anophelis_g	
25	446.5	19.5	146	2	Q6Q450_DROBU
26	277	12.1	49	2	Q65918_HUMAN
27	254	11.5	75	2	Q5M03_CHICK
28	212	9.3	57	2	Q4RAV6_TEING
29	122.5	5.3	215	2	Q9YV18_MSIRPV
30	119	5.2	340	2	Q8VX5_ENGCC
31	1358	5.2	Q7QC06_ANOGA		

### ALIGNMENTS

RESULT 1	PELI2_HUMAN	STANDARD;	PRT;	420 AA.
ID	PELI2_HUMAN			
AC	QHATB			
DT	29-MAR-2004 (Rel. 43, Created)			
DT	28-MAR-2004 (Rel. 43, Last Sequence update)			
DR	Pellino protein homolog 2 (Pellino 2).			
GN	Name=PEL12;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
OC				
OU				
RN				
RP	NUCLEOTIDE SEQUENCE.			
RK	MEDLINE-2120370; PubMed-11306823;			
RA	Kesch K., Jockusch H., Schmitt-John T.,			
RA	"Assignment of homologous genes, Peli1/PELI1 and Peli2/PELI2, for the Pelle adaptor protein Pellino 1 to mouse chromosomes 11 and 14 and human chromosomes 2p13.3 and 14q21, respectively, by physical and radiation hybrid mapping.";			
RT	Pelle adaptor protein Pellino 1 to mouse chromosomes 11 and 14 and human chromosomes 2p13.3 and 14q21, respectively, by physical and radiation hybrid mapping.			
RU	Otogeneet..Cell. Genet., 92:172-174 (2001).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].			
RC	TISSUE-LUNG.			
RA	Strausberg R.L., Feingold E.A., Gruber L.H., Berger J.G., Schuler G.D., Klausner R.D., Colling R.S., Wagner L., Shemesh C.M., Schueler B., Bhat N.K., Altschul S.F., Zeeberg B., Buettner K.H., Schaeffer C.P., Bhattacharjee A., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F., Diatchenko L., Matsunaga K., Farmer A.R., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldio M.F., Casavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frangie C., Raha S., Joquielano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villafron D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A., Farney J.J., Heitton E., Ketteman M., Macian A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shvechenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Sanger R., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RT	and mouse cDNA sequences."			
RU	Proc. Natl. Acad. Sci. U.S.A., 99:16999-15903(2002).			
RN	[3]			
RP	FUNCTION, AND INTERACTIONS WITH TRAF6 AND MAP3K7.			
RA	MEDLINE-22689054; PubMed-2804775; DOI-10.1016/S0014-5793(03)00533-7;			
RA	Jensen L.E., Whitehead A.S.;			
RT	"Pellino2 activates the mitogen activated protein kinase pathway."			
RA	FERS Lett. 545:199-202(2003).			
RN	[4]			

RP FUNCTION, PROSPHORYLATION, AND INTERACTIONS WITH IRAK1 AND IRAK4.  
 RX MEDLINE=2274764; PubMed=12860450; DOI=10.1016/S0014-5792(03)00697-5;  
 RA Sreelow A., Kollewe C., Weiche H.;  
 RT Characterization of Pellino2, a substrate of IRAK1 and IRAK4.;  
 RL FEBS Lett. 547:157-161(2003).  
 CC -I- FUNCTION: Scaffold protein which probably links Toll-like  
 receptors (TIRs) to basic cellular processes via its interaction  
 with the complex containing IRAK kinases and TRAF6. Can activate  
 the MAP (mitogen activated protein) kinase pathway leading to  
 activation of ERK1. Not required for NF-kappa-B activation.  
 CC -I- SUBUNIT: Interacts with TRAF6, IRAK1, IRAK4 and MAP3K7.  
 CC -I- INTERACTION:  
 PS1617-IRAK1; NBExp=1; Intact=EBI-448407; EBI-558664;  
 Q9NWZ3;IRAK4; NBExp=1; Intact=EBI-448407; EBI-448378;  
 CC -I- PTM: Phosphylated by IRAK1 and IRAK4.  
 CC -I- SIMILARITY: Belongs to the pellino family.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 CC EMBL; AF302502; AAG15390.1; -; mRNA.  
 DR EMBL; BC009476; AAH09476.1; -; mRNA.  
 DR INACT; Q9HATB; -;  
 DR Ensembl; ENSG0000139946; Homo sapiens.  
 DR HGNC:8828; PELT2.  
 DR InvDB; HKX001690; -;  
 DR InterPro; IPR006000; -;  
 DR PANTHER; PTHR1208; Pellino; 1.  
 DR Pfam; PF04710; Pellino; 1.  
 DR RPSBQSEQUENCE; 420 AA; 46435 MW; 2FC5E661C13BC11A CRC64;  
 Query Match Best Local Similarity 100.0%; Score 2290; DB 1; Length 420;  
 Matches 420; Conservative 0; Mismatches 0; Indels 0; GapB 0;  
 Qy 1 MSpGQEHCPAHPKEPVKGELVYNGALPGDRGRKSRLALKRKPCKANVCPSTH 60  
 Db 1 MSpGQEHCPAHPKEPVKGELVYNGALPGDRGRKSRLALKRKPCKANVCPSTH 60  
 Qy 61 VISTPOASKAIACKGHSITSYTSRNQTVWETHDKOTDMQGRSTBSPDPFWDTI 120  
 Db 61 VISTPOASKAIACKGHSITSYTSRNQTVWETHDKOTDMQGRSTBSPDPFWDTI 120  
 Qy 121 SGSQNTDQAQTOSTISRFACR1VCDRNPYPTARIIFAAAGFDSSRNIFLGEKAKWKPDG 180  
 Db 121 SGSONTDEAQITOSTISRFACR1VCDRNPYPTARIIFAAAGFDSSRNIFLGEKAKWKPDG 180  
 Qy 181 HMDGLITTINGVLMIPRGQTEESQPGVWRBISVGDVYLRETRSAORGKVVESETNVL 240  
 Db 181 HMDGLITTINGVLMIPRGQTEESQPGVWRBISVGDVYLRETRSAORGKVVESETNVL 240  
 Qy 241 QDSSLIDGATIILWRTADGLPHTPTOKHIELRQEINARPQCPVGLNTAPPSTINKE 300  
 Db 241 QDSSLIDGATIILWRTADGLPHTPTOKHIELRQEINARPQCPVGLNTAPPSTINKE 300  
 Qy 301 VVZEKQPMAYLSCHVGHYHNWHGRSDTEANERBRCPMCRTVGVYVPLMGCEAGFYTDG 360  
 Db 301 VVZEKQPMAYLSCHVGHYHNWHGRSDTEANERBRCPMCRTVGVYVPLMGCEAGFYTDG 360  
 Qy 361 PPTHAFTTCGHVSEKSKCWSOPLPRTGTHAHCPCATOLVGEONCNULFOCPID 420  
 Db 361 PPTHAFTTCGHVSEKSKCWSOPLPRTGTHAHCPCATOLVGEONCNULFOCPID 420  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DT Pellino protein homolog 2 (Pellino 2).  
 GN Name=Peli2;  
 OS Mus musculus (Mouse);  
 OC Mammalia; Rutheria; Buarchoontoglires; Gires; Rodentia; Sciurognathi;  
 OC Muroidea; Muridae; Murinae; Mus;  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RC STRAIN=C57BL/6J;  
 RN MEDLINE=21203570; PubMed=11306823;  
 RC REBCH K., Jockusch H., Schmitt-John T.;  
 RN "Assignment of homologous genes, Peli2/PELI2, for the  
 Pelle adaptor protein, Pellino to mouse chromosomes 11 and 14 and human  
 chromosomes 2p13.3 and 14q21, respectively, by physical and radiation  
 hybrid mapping";  
 RC Cytogenet. Cell Genet. 92:172-174(2001).  
 [2]  
 RN NUCLEOTIDE SEQUENCE (LARGE SCALE RNA) (ISOFORMS 1 AND 3).  
 RC STRAIN=C57BL/6J; TISSUE=Corebellum, Epididymis, and Pituitary;  
 RN MEDLINE=22254683; PubMed=1246651; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kubakawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamamoto I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nomami A., Schonbach C., Gejohori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Nogami A., Schonbach C., Gejohori T.,  
 RA Schrinil L.M., Kanapin A., Masuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,  
 RA Dalla R., Dragani T.A., Fletcher C., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmer S.D., Guicciardini S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurouchkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavon W.J., Peretea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Oi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang J., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hikozane-Kubikawa T., Kounio H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arkawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Inotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sakai D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs";  
 RN Nature 420:563-573 (2002).  
 [3]  
 RN NUCLEOTIDE SEQUENCE (LARGE SCALE RNA) (ISOFORM 2).  
 RC TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubhaar R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Sheppard C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heile F.,  
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiriki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McBain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Farhey J., Helton E., Kettman M.C., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimm S., Schmutz J.H., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska M., Smailus D.E.,  
 RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RESULT 2

PEL12\_MOUSE STANDARD; PRT; 419 AA.

ID PEL12\_MOUSE STANDARD; PRT; 419 AA.

ID 088B5T6; Q8CCF2; Q8CCG5; Q8R2X4; Q8ERJ7; DT 29-MAR-2004 (Rel. 43, Created)

"Generation and initial analysis of more than 15,000 full-length human RT  
 RT and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002).  
 RN [4]  
 RP FUNCTION, TISSUE SPECIFICITY, AND INTERACTION WITH IRAK1.  
 RX MEDLINE=2257640; PubMed=12370331;  
 RA Yu K.-Y.; Kwon H.-J.; Norman D.A.M.; Vig E.; Goebel M.G.,  
 Harrington M.A.;  
 RT "Mouse Pellino-2 modulates IL-1 and lipopolysaccharide signaling.";  
 RL J. Immunol. 169:4075-4078(2002);  
 CC -- FUNCTION: Scaffold protein which probably links Toll-like receptors (TLRs) to basic cellular processes via its interaction with the complex containing IRAK kinases and TRAF6. Can activate the MAP (mitogen activated protein) kinase pathway leading to activation of ERK1. Not required for NF-kappa-B activation.  
 CC -- SUBUNIT: Interacts with TRAF6, IRAK4 and MAP3K7 (BY SIMILARITY).  
 CC -- INTERACTION:  
 CC -0624061rakl; Nbsxplc1; Intact=EBI-448554, EBI-448533;  
 CC -- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative Splicing; Named isoforms=3;  
 CC Iso1=Q8BS76-1; SequenceDisplayed;  
 CC Name=2; Iso1=Q8BS76-2; Sequence=VSP\_008635;  
 CC Note=No experimental confirmation available;  
 CC Name=3; Iso1=Q8BS76-3; Sequence=VSP\_008637, VSP\_008638;  
 CC Note=No experimental confirmation available;  
 CC -- TISSUE SPECIFICITY: Widely expressed both in embryos and adult.  
 CC -- PTM: Phosphorylated weakly or not expressed in spleen and thymus.  
 CC -- SIMILARITY: Belongs to the Pellino family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.  
 CC  
 CC  
 CC DR AF302504; AA913392.1; -; mRNA.  
 DR EMBL: AK030564; BAC2024.1; -; mRNA.  
 DR EMBL; AK030564; BAC2024.1; -; mRNA.  
 DR EMBL: AK082342; BAC31472.1; -; mRNA.  
 DR EMBL; BC2062; AH21062.1; -; mRNA.  
 DR INTACT; Q8BS76; -;  
 DR Ensembl; ENSMUSG00000021846; Mus musculus.  
 DR MGI; MGI:1891445; Pel12.  
 GO; GO:000515; P:protein binding; IPI.  
 DR InterPro; IPR005800; Pellino.  
 DR PANTHER; PTMR12088; Pellino; 1.  
 DR PR04710; Pellino; 1.  
 KW Alternative splicing; Phosphorylation.  
 FT VARSPLIC 1 100 Missing (in isoform 2).  
 FT /FTid=VSP\_008636.  
 FT VARSPLIC 70 155 ASSRGHSTSYTSLRSOTWVVEYTHDKTDWQGRSTES  
 FT PDFFVVTGSGQNEAQDQTSTISFRCVCDRNEPPT  
 FT ARIFP -> LPACKHYVNADSSLSAATLKVDPLTCECSQ  
 FT REYRPDPASRPGSAGSQAQLQAFICPLSTIVKOBQIR  
 FT CUKKPKFSCWS (in isoform 3).  
 FT /FTid=VSP\_008637.  
 FT VARSPLIC 156 419 Missing (In isoform 3).  
 FT /FTid=VSP\_008638.  
 FT CONFLICT 7 7 E -> K (in Ref. 2; BAC27024).  
 FT CONFLICT 11 11 A -> T (in Ref. 2; BAC27024).  
 FT CONFLICT 20 20 R -> G (in Ref. 2; BAC28472).  
 FT CONFLICT 39 39 R -> KK (in Ref. 1).  
 FT CONFLICT 44 44 A -> T (in Ref. 1).  
 FT CONFLICT 320 320 S -> H (in Ref. 1).  
 FT CONFLICT 327 327 T -> A (in Ref. 3).  
 FT CONFLICT 338 338 R -> M (in Ref. 1).  
 FT CONFLICT 364 364 A -> V (in Ref. 1).  
 FT CONFLICT 419 419 AA; 46272 MM; 786C92C28C38D0CB CRG64;

RESULT 3  
 O6GQ57\_XENLA  
 ID O6GQ57\_XENLA PRELIMINARY; PRT; 419 AA.  
 AC 06GQ57  
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, last sequence update)  
 DB MGCB0329 protein.  
 GN Name=MGCB0329;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bivalvia; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopidae; Xenopus; Xenopus.  
 OX NCBI\_TAXID=8355,  
 RN [1]  
 RP NUCBLDDB SEQUENCE.  
 RC TISSUE=Ovary;  
 MEDLINE=2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Colline P.S., Wagner L., Shemesh C.M., Schubert G.D.,  
 RA Altschul S.P., Zeeberg B., Bustow K.H., Schaeffer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heilek F.,  
 RA Diatchenko L., Matsunaga K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schatz T.B.,  
 RA Brownstein M.J., Usdin T.B., Toshiriki S., Carninci P., Prange C.,  
 RA Raha S.A., Loquai Lano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzyk D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettemann M., Madden A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Tuchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.N.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smialius D.E.,  
 RA Scherzer A., Schein J.B., Jones S.J.M., Marr M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002).  
 RN [2]

R P NUCLEOTIDE SEQUENCE.  
 RC TISSUE=ovary;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.; "genomic and genetic tools for Xenopus research: The NIH Xenopus  
 RT initiative"; Dev. Dyn. 225:384-391(2002).  
 RL [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=ovary;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (TUN-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC072891; AAH72891.1; -; mRNA.  
 DR InterPro; IPR006800; Pellino.  
 DR Pfam; PF04710; Pellino; 1.  
 SQ SEQUENCE 419 AA; 46372 MW; 55AC2FE7953D6145 CRC64;

Query Match 93.4%; Score 2138.5; DB 2; Length 419;  
 Best Local Similarity 91.2%; Pred. No. 5.6e-170; Mismatches 12; Indels 1; Gaps 1;  
 Matches 383; Conservative 24; MisMatches 12; Indels 1;

OY 1 MFSPGQEBEHCAPNKEPKVKGELVWLYNGALPNQDRGRKSRALYKPKRANKVKPSTVH 60  
 Db 1 MFSPGQEBEHCAPNKEPKVKGELVWLYNGALPNQDRGRKSRALYKPKRANKVKPSTVH 60  
 OY 61 VISPTQASKAISCKGQHSISYTTSRNQTVVWYTHDKDTDMFOVGRSTESPIDFVVTDTI 120  
 Db 61 VISPTQASKAISCKGQHSISYTTSRNQTVVWYTHDKDTDMFOVGRSTESPIDFVVTDTI 120  
 OY 121 SGSONTDEAQITQSTISRFACRIVCDRNPYTAIFAGPDSKNIPLGEKAKWKNDP 180  
 Db 121 SGSONTDEAQITQSTISRFACRIVCDRNPYTAIFAGPDSKNIPLGEKAKWKNDP 180  
 OY 181 HMDGLTTNGVLUVMHPKGFTESOPGVWREISVCGDVTILRETSAQORGKLVESETVNL 240  
 Db 180 HMDGLTTNGVLUVMHPKGFTESOPGVWREISVCGDVTILRETSAQORGKLVESETVNL 240  
 OY 241 QDSSLIDIGATLWRTADGLHTPTOKHIAEALRQEINARPOCPVGLNTLAPPNSRKD 299  
 Db 240 QDSSLIDIGATLWRTADGLHTPTOKHIAEALRQEINARPOCPVGLNTLAPPNSRKD 299  
 OY 301 VWEKQPMAYLSCGHVYGHYNGHRSDETEANERBCPMCTGVPYVPLMGCEAGFYVDG 360  
 Db 300 VWEKQPMAYLSCGHVYGHYNGHRSDETEANERBCPMCTGVPYVPLMGCEAGFYVDG 360  
 OY 361 PPTHAFTPCGHVSESEKSAKWSQIPLPHTAFAACPCATQOLVGEONCILQFOGRID 420  
 Db 360 PPTHAFTPCGHVSESEKSAKWSQIPLPHTAFAACPCATQOLVGEONCILQFOGRID 420  
 RESULT 4  
 QP4Y5 XENTR PRELIMINARY; PRT; 419 AA.  
 AC QP4Y5;  
 DT 05-JUL-2004 (TREMBrel. 27, Created)  
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)  
 DE Hypothetical protein MGC75650.  
 GN Name=MGC75650;  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Amphibia; Batrachia; Amura; Mesobatrachia; Pipoidea; Pipidae;  
 OC Xenopodinae; Xenopus; Silurana.  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22380257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Submitted (TUN-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; BC072891; AAH72891.1; -; mRNA.  
 DR InterPro; IPR006800; Pellino.  
 DR Pfam; PF04710; Pellino; 1.  
 SQ SEQUENCE 419 AA; 46372 MW; 55AC2FE7953D6145 CRC64;

Query Match 93.4%; Score 2138.5; DB 2; Length 419;  
 Best Local Similarity 91.2%; Pred. No. 5.6e-170; Mismatches 12; Indels 1; Gaps 1;  
 Matches 383; Conservative 24; MisMatches 12; Indels 1;

OY 1 MFSPGQEBEHCAPNKEPKVKGELVWLYNGALPNQDRGRKSRALYKPKRANKVKPSTVH 60  
 Db 1 MFSPGQEBEHCAPNKEPKVKGELVWLYNGALPNQDRGRKSRALYKPKRANKVKPSTVH 60  
 OY 61 VISPTQASKAISCKGQHSISYTTSRNQTVVWYTHDKDTDMFOVGRSTESPIDFVVTDTI 120  
 Db 61 VISPTQASKAISCKGQHSISYTTSRNQTVVWYTHDKDTDMFOVGRSTESPIDFVVTDTI 120  
 OY 121 SGSONTDEAQITQSTISRFACRIVCDRNPYTAIFAGPDSKNIPLGEKAKWKNDP 180  
 Db 121 SGSONTDEAQITQSTISRFACRIVCDRNPYTAIFAGPDSKNIPLGEKAKWKNDP 180  
 OY 181 HMDGLTTNGVLUVMHPKGFTESOPGVWREISVCGDVTILRETSAQORGKLVESETVNL 240  
 Db 180 HMDGLTTNGVLUVMHPKGFTESOPGVWREISVCGDVTILRETSAQORGKLVESETVNL 240  
 OY 241 QDSSLIDIGATLWRTADGLHTPTOKHIAEALRQEINARPOCPVGLNTLAPPNSRKD 299  
 Db 240 QDSSLIDIGATLWRTADGLHTPTOKHIAEALRQEINARPOCPVGLNTLAPPNSRKD 299  
 OY 301 VWEKQPMAYLSCGHVYGHYNGHRSDETEANERBCPMCTGVPYVPLMGCEAGFYVDG 360  
 Db 300 VWEKQPMAYLSCGHVYGHYNGHRSDETEANERBCPMCTGVPYVPLMGCEAGFYVDG 360  
 OY 361 PPTHAFTPCGHVSESEKSAKWSQIPLPHTAFAACPCATQOLVGEONCILQFOGRID 420  
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 RESULT 5  
 QDHB8 BRARE PRELIMINARY; PRT; 428 AA.  
 AC QDHB8;  
 DT 25-OCT-2004 (TREMBrel. 28, Created)  
 DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)  
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)  
 DE Pellino homolog 2.  
 GN Name=pel12;  
 OS Brachyuryo rerio (zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Actinopterygii; Neoperrygii; Teleosteii; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.

OK NCBI\_TAXID=7955;  
 RN [1]  
 RP NUCLEOTIDE\_SEQUENCE.  
 RX TISSUE=Whole;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Peingold E.A., Grouse L.H., Derge J.G.,  
 Strauberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Altenschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 Hopkins R.P., Jordan H., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Caminici P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,  
 Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.B.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.",  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP NUCLEOTIDE\_SEQUENCE.  
 RC TISSUE=Whole;  
 RG NIH\_MGC\_Project;  
 RL Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL: BC075973; ARH75973.1; -; mRNA.  
 DR ZFIN: ZDB-GENE-050718-360; zgc:92268.  
 DR InterPro: IPR006900; Pellino.  
 DR Pfam: PF04710; Pellino\_1.  
 DR SEQUENCE 428 AA; 47287 MW; B3389084 9BF4366A CRC64;

Query Match 87.6%; Score 2006; DB 2; Length 428;  
 Best Local Similarity 84.3%; Pred. No. 8.1e-159;  
 Matches 361; Conservative 28; Mismatches 31; Indels 8; Gaps 2;

QV 1 MFSPGQEEBHCAPANCPVKYGVLYGALPNQDRGRKSRFLAKYKPKANGVKPSTVH 60  
 Db 1 MFSPGQEEBHCAPANCPVKYGVLYGALPNQDRGRKSRFLAKYKPKANGVKPSTVH 60  
 RA Straussberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Caminici P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,  
 Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.B.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.",  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [3]  
 RP NUCLEOTIDE\_SEQUENCE.  
 RC TISSUE=Thymus;  
 MEDLINE=21015032; PubMed=11132151; DOI=10.1007/s002510000249;  
 RA Rich T., Allen R.L., Lucas A.M., Trowsdale J.;  
 RT Pellino-related sequences from *Caenorhabditis elegans* and *Homo  
 sapiens*.;  
 RT Immunogenetics 52:145-149(2000).  
 RL Immunogenetics 52:145-149(2000).  
 RN [4]  
 RP NUCLEOTIDE\_SEQUENCE.  
 RC MEDLINE=21203570; PubMed=111306923;  
 RA Reach K., Jockusch H., Schmitt John T.;  
 RT Assignment of homologous genes, Pellini and Pelii/PELL2, for the  
 Pelle adaptor Protein Pellini to mouse chromosomes 11 and 14 and human  
 chromosomes 2p13.3 and 1q21, respectively, by physical and radiation  
 hybrid mapping.  
 RT Cytogenet. Cell. Genet. 92:172-174(2001).  
 RN [5]  
 RP NUCLEOTIDE\_SEQUENCE.  
 RA Kennedy E.J., Monagh P.N.;  
 RT PRISM, a novel mediator of Toll/IL-1 signalling.;  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.  
 RN NUCLEOTIDE\_SEQUENCE [LARGE SCALE MANUAL].  
 RC TISSUE=Ovary, Placenta, and Testis;  
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
 Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Usdin T.B., Toshiyuki S., Caminici P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J.,  
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Guy L.J., Hulyk S.W.,  
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 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.B.,  
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.",  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN NUCLEOTIDE\_SEQUENCE [LARGE SCALE MANUAL] OF 78-418.  
 RC TISSUE=Mteratocarcinoma;  
 MEDLINE=14702039; PubMed=10.1038/ng1285;  
 RA Ota T., Suzuki Y., Nishikata T., Otsuki T., Sugiyama T., Irie R.,  
 Wakamatsu K., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,  
 Sekine M., Obayashi M., Nishi T., Shibakawa T., Tanaka T., Ishii S.,  
 Yamamoto J.-I., Saito Y., Kawai Y., Isomo Y., Nakamura Y.,  
 Nagahara K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,  
 Shiratori A., Sudou H., Hosokiri T., Kaku Y., Kodaira H., Kondo H.,  
 Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,  
 Omura Y., Abe K., Kamihara K., Katsuma N., Sato K., Tanikawa M.,





Db	119	PSSQSNISDTQSIVQSTISRFACTRTERSPPTRARYAGFDSSKNTIFLGEKAARKTKTSQG	178	RESULT 10
QY	181	HMDGLITTGVLVLMRPGGTEESQGVWRBISVGCDVYLTRETAQORGKLVESTBNVL	240	Q7ZKU3_XENLA PRELIMINARY; PRT; 418 AA.
Db	179	QMDGLITTGVLVLMRPGGTEESQGVWRBISVGCDVYLTRETAQORGKLVESTBNVL	240	Q7ZKU3_XENLA PRELIMINARY; PRT; 418 AA.
QY	241	QDSSLIDLGATIILWRTADGLFTPTQKTHAQLRQPINARPOCPGQNLAFASSNRGE	300	07ZKU3_XENLA PRELIMINARY; PRT; 418 AA.
Db	239	QDSSLIDLGATIILWRTADGLFTPTQKTHAQLRQPINARPOCPGQNLAFASSNRGE	300	07ZKU3_XENLA PRELIMINARY; PRT; 418 AA.
QY	301	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG	360	01-JUN-2003 (TREMBlrel. 24, Last sequence update)
Db	299	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG	360	01-OCT-2003 (TREMBlrel. 25, Last annotation update)
QY	361	PPTHTAFTPCCGHVCSSEKSAKWSOFLPFLGTHAFHACPPCATOLWGEONCKLKFQGPID	420	DB_Pell-pro protein.
Db	359	PPTHTAFTPCCGHVCSSEKSAKWSOFLPFLGTHAFHACPPCAHQLAGEOGYIRLIRFGPLD	418	Xenopus laevis (African clawed frog).
QY	301	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG	360	OS_Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Amnia; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Xenopus; Xenopus.
OC				NCBI_TaxID=8355;
OX				[1]
RN				RP_NUCLEOTIDE SEQUENCE.
RC				TISSUE=Embryo;
RX				MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA				Klauser R.D., Collins P.S., Wagner L., Grouse L.H., Derree J.G., Schuler G.D., Strausberg R.L., Fengoid E.A., Grouse L.H., Shearer C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bluetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Borodko M.F., Caravant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarine P.H., Richards S., Worley K.C., Hale S., Garcia E.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Keeteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko I., Bouffard G.G., Blakesley R.W., Touchman J.W., Graen E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., NCBI_TAXID=10090;
RA				Rodriguez Y.S.N., Kitzwinski M.I., Skalska U.R., Smailus D.B., Schnierch A., Schein J.E., Jones J.S.M., Marra M.A., RT_and mouse cDNA sequences;" Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RA				RT_RN [2]
RA				RP_NUCLEOTIDE SEQUENCE.
RX				TISSUE=Embryo;
RA				MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA				Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative"; Dev. Dyn. 225:384-391 (2002).
RA				RT_RL RN [3]
RA				RP_NUCLEOTIDE SEQUENCE.
RA				TISSUE=Embryo;
RA				Klein S., Strausberg R.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative"; Dev. Dyn. 225:384-391 (2002).
RA				RT_RL DR_InterPro; IPRO06800; Pellino.
DR				PFam; PF04710; Pellino; 1.
DR				DR_SEQUENCE; 418 AA; 46231 MW; 04DCFP12560BAD530 CRC64;
DR				DR_SEQUENCE; 418 AA; 46231 MW; 04DCFP12560BAD530 CRC64;
QY	181	HMDGLITTGVLVLMRPGGTEESQGVWRBISVGCDVYLTRETAQORGKLVESTBNVL	240	Query Match, Best Local Similarity 82.3%; Score 1884; DB 2; Length 418; Matches 338; Conservative 80.5%; Pred. No. 1.2e-148; Indels 2; Gaps 1;
Db	179	QMDGLITTGVLVLMRPGGTEESQGVWRBISVGCDVYLTRETAQORGKLVESTBNVL	238	QMDGLITTGVLVLMRPGGTEESQGVWRBISVGCDVYLTRETAQORGKLVESTBNVL
QY	241	QDSSLIDLGATIILWRTADGLFTPTQKTHAQLRQPINARPOCPGQNLAFASSNRGE	300	QDSSLIDLGATIILWRTADGLFTPTQKTHAQLRQPINARPOCPGQNLAFASSNRGE
Db	239	QDSSLIDLGATIILWRTADGLFTPTQKTHAQLRQPINARPOCPGQNLAFASSNRGE	298	QDSSLIDLGATIILWRTADGLFTPTQKTHAQLRQPINARPOCPGQNLAFASSNRGE
QY	301	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG	360	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG
Db	299	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG	358	VWEKQPMWYLSCCHVHGHNWHRSDETEANERCPMCRTGVPVPLMGCEAGFVYDAG
QY	361	PPTHTAFTPCCGHVCSSEKSAKWSOFLPFLGTHAFHACPPCATOLWGEONCKLKFQGPID	420	PPTHTAFTPCCGHVCSSEKSAKWSOFLPFLGTHAFHACPPCATOLWGEONCKLKFQGPID
Db	359	PPTHTAFTPCCGHVCSSEKSAKWSOFLPFLGTHAFHACPPCATOLWGEONCKLKFQGPID	418	PPTHTAFTPCCGHVCSSEKSAKWSOFLPFLGTHAFHACPPCATOLWGEONCKLKFQGPID

Db	179	QMDGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL	OY	361	PPTHAFTPCGHVCSEKAKYKWSQIPLDHGTAAACPFCAOLVGB
OY	241	QDSLSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSINKE	Db	359	PPTHAFTPCGHVCSEKAKYKWSQIPLDHGTAAACPFCAOLAGE
Db	239	QDSLSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSKRD	OY	301	VVEBKOPWAVLSCGHVHGTHNGHRSDTBANERECPMRTVSGVPUMLGCRAGFYTDAG
Db	299	VVDKQPAWVLYNCGHVHGHNWKERDGKDRCPMGRSVGPVPLNGCFAFYDAG	Db	358	VVEBKOPWAVLSCGHVHGTHNGHRSDTBANERECPMRTVSGVPUMLGCRAGFYTDAG
OY	361	PPTHAFTPCGHVCSEKAKYKWSQIPLDHGTAAACPFCAOLVGB	Db	359	PPTHAFTPCGHVCSEKAKYKWSQIPLDHGTAAACPFCAOLAGE
Db	359	PPTHAFTPCGHVCSEKAKYKWSQIPLDHGTAAACPFCAOLAGE	OY	359	PPTHAFTPCGHVCSEKAKYKWSQIPLDHGTAAACPFCAOLAGE
RESULT 11			RESULT 12		
ID 052KT7, CHICK PRELIMINARY;	PRT;	405 AA.	ID QSGC9, TETNG		
AC 052KT7;			ID QSGC9, TETNG PRELIMINARY;	PRT;	428 AA.
DT 25-OCT-2004 (TREMBREL. 28, Created)			AC QSGC9;		
DT 25-OCT-2004 (TREMBREL. 28, Last sequence update)			DT QSGC9;		
DE Hypothetical protein.			DT 13-SEP-2005 (TREMBREL. 31, Last sequence update)		
GN ORFNames=RCBmB04_9d4;			DB 13-SEP-2005 (TREMBREL. 31, Last annotation update)		
OS Gallus gallus (Chicken).			GN Chromosome 17 SCF14587, whole genome shotgun sequence.		
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			OS ORFNames=GSTENG00101870101.		
OC Gallus.			OS Tetraodon nigroviridis (Green puffer).		
OK NCBITaxID=9031;			OC Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Osteichthyes; Tetradontidae; Tetraodon.		
RN [1]			OC Anthomorpha; Actanthopterygii; Percormorpha; Teleostei; Tetradontidae; Tetraodontidae; Tetraodon.		
RP NUCLEOTIDE SEQUENCE.			OK NCBITaxID=99883;		
RC STRAIN-CB, TISSUE-Bursa;			RN Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,		
RA Fiedler P., Kutter S., Bladostatski A.M., Kostovska D., Kotter M.,			RA Mauceli E., Boureau L., Fischer C., Ozouf-Costaz C., Bernot A.,		
RA Plachy J., Carnici P., Hayashita Y., Blairstedde J.M.,			RA Niclaid S., Jaffe D., Fisher S., Luttrilla G., Dossat C., Segurens B.,		
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate genefunction analysis";			RA Desilva C., Salamoutab M., Levy M., Boudet N., Castellano S.,		
RL Genome Biol 6:R6 (2005).			RA Anthorard V., Jubin C., Castelli V., Katinka M., Vacherie B.,		
DR InterPro; IPR006200; Pelliino.			RA Bleumont C., Skalnik Z., Cattolico L., Poulin J., de Berardini's V.,		
DR InterPro; IPR04710; Pelliino.			RA Cruaud C., Duprat S., Brodtier P., Coutanceau J.-P., Gouzy J.,		
KW Hypothetical protein.			RA Parra G., Lardier G., Chapelle C., McEwan P., Bosak S.,		
SQ SEQUENCE 405 AA; 44790 MW; 8928FB5EP52DB3BF CRC64;			RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,		
Query Match Best Local Similarity 81.4%; Score 1864; DB 2; Length 405; Matches 333; Conservative 36; Mismatches 35; Indels 2; Gaps 1;			RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,		
OY 1 MFSPGQEEHCAPNKEPVKYGELVUWLGNGALPNDRGRKSRLAFLYKPKANGVKSTH			RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,		
Db 1 MFSPQDOENH-PSKAPVKYGEIWLVLGNGSLPNDRGRKSRLAFLYKPKANGVKSTH			RA Wincker P., Lander E.S., Weissenbach J., Roest Croilius H.,		
OY 61 VISTPQAQKAISSCKQHSISITSLRQNTOVWEITHDKOTDMQVRGTSRESPDFWVTDI			RT the early vertebrate proto-karyotype.",		
Db 59 IACTPQAQKAISSCKQHSISITSLRQNTOVWEITHDSWMDMQRGTSRESPDFWVTDI			RT Nature 431:946-957 (2004).		
OY 121 SSQONTDAQTOSTISPARC1VCDRNPYTTARIIFAGFDSSKRKNPILGEKAQKWNPDG			RN [2]		
Db 119 PEGQSNSTQSTOSVOSTISPARC1CERPPFTRIYAFGFDSSKNIIGEKAKWTSQ			RP NUCLEOTIDE SEQUENCE.		
OY 181 HDGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL			RC Genoscope; Whitehead Institute Centre for Genome Research;		
Db 179 QMDGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL			CC Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.		
OY 241 QDSLSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSINKE			CC -1- CATION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.		
Db 239 QDSLSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSINKE			DR EMBL; CKA0101497; CG00303.1, -, Genomic DNA.		
OY 301 VVEBKOPWAVLSCGHVHGTHNGHRSDTBANERECPMRTVSGVPUMLGCRAGFYTDAG			SQ SEQUENCE 428 AA; 47639 MW; B4187096D4454577 CRC64;		
Db 299 VVEBKOPWAVLSCGHVHGTHNGHRSDTBANERECPMRTVSGVPUMLGCRAGFYTDAG			Query Match Best Local Similarity 78.1%; Score 1788; DB 2; Length 428; Matches 329; Conservative 38; Mismatches 53; Indels 8; Gaps 3;		
OY 1 MFSPGQOB-EHCAPNKEPVKYGELVUWLGNGALPNDRGRKSRLAFLYKPKANGVKST			Matches 329; Conservative 38; Mismatches 53; Indels 8; Gaps 3;		
Db 59 VVISTPQAQKAISSCKQHSISITSLRQNTOVWEITHDKOTDMQVRGTSRESPDFWVTDI			OY 1 MFSPGQOB-EHCAPNKEPVKYGELVUWLGNGALPNDRGRKSRLAFLYKPKANGVKST		
OY 121 SSQONTDAQTOSTISPARC1VCDRNPYTTARIIFAGFDSSKRKNPILGEKAQKWNPDG			Db 59 VVISTPQAQKAISSCKQHSISITSLRQNTOVWEITHDKOTDMQVRGTSRESPDFWVTDI		
Db 119 PEGQSNSTQSTOSVOSTISPARC1CERPPFTRIYAFGFDSSKNIIGEKAKWTSQ			OY 61 VHACSPQAQKAISSCKQHSISITSLRQNTOVWEITHDSWMDMQRGTSRESPDFWVTDI		
OY 181 HDGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL			Db 119 TTSQONTRDAQTOSTISPARC1CERPPFTRIYAFGFDSSKNIIGEKAKWTSQ		
Db 179 QMDGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL			Db 121 TVAGSHSNTDGTGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSI		
OY 241 QDSLSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSINKE			OY 177 NPDMGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL		
Db 239 QDSLSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSINKE			Db 181 TFGQMDGLITTINGVLUWPRKGRTPEFTEDSKPGVWRREISVGNGNFSLRETRSAORGKWTENSTL		
OY 301 VVEBKOPWAVLSCGHVHGTHNGHRSDTBANERECPMRTVSGVPUMLGCRAGFYTDAG			Db 237 TVAGSHSNTDGTGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSI		
Db 299 VVEBKOPWAVLSCGHVHGTHNGHRSDTBANERECPMRTVSGVPUMLGCRAGFYTDAG			OY 241 SHDSLIDGATIWLRTADGLFTPTKIRALRQEINARPOCPVGNTLAFFPSM		
OY 358			Db 298		

Db	301	HRKDTPDEKOPWPWYIQCQGHVHGYYHNGNPREEREGREGDRDRECPMPCRTKGYPVPLWLGC	360
Oy	353	AGEFTDAGPTAATPGCGTCSERAKYMSQIPRHGTHAFACPPCATOLVGNCIK	412
Db	361	AGPYTDAAFPHTAFSPCGHVCEKTAAYNSQIPLPHGTIFHAACPFCAHOLSIDQGYVR	420
Oy	413	LIFQGPID	420
Db	421	LIFQGPID	428
RESULT 13			
ID	Q4SBZL_TETNG	TETNG PRELIMINARY;	PRT; 440 AA.
ID	Q4SBZL	TETNG PRELIMINARY;	PRT; 440 AA.
AC	Q4SBZL	TETNG PRELIMINARY;	PRT; 440 AA.
AC	Q4SBZL	TETNG PRELIMINARY;	PRT; 440 AA.
DT	13-SEP-2005	(Tremblrel. 31, Last sequence update)	
DT	13-SEP-2005	(Tremblrel. 31, Last annotation update)	
DE	Chromosome 14 SCAF14660	whole genome shotgun sequence.	
DE	(Fragment).		
GN	ORFName=GSTENGG00020745001;		
OS	Tetraodon nigroviridis (Green puffer).		
OS	Tetraodon nigroviridis (Green puffer).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodon.		
OX	NCBI_TAXID=99883;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Jailion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,		
RA	Mauclaire E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,		
RA	Duclos S., Jaffe D., Fisher S., Lutfalla M., Doseat C., Segurens B.,		
RA	Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,		
RA	Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,		
RA	Biémont C., Skalli Z., Cattolico L., Pouain J., De Bernardini V.,		
RA	Cruaud C., Dupratt S., Brottier P., Courtaudon J., Pe Gouzy J.,		
RA	Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,		
RA	Kelis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J., Robinson-Richards M.,		
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,		
RA	Laudet V., Schachter V., Quétier F., Saurin W., Scarpelli C.,		
RA	Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,		
RA	"Genomic duplication in the teleost fish Tetraodon nigroviridis reveals		
RT	the early vertebrate proto-karyotype.";		
RL	Nature 431:946-957(2004).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RG	Genoscope; Whitehead Institute Centre for Genome Research;		
RL	Submitted (FB2004) to the EMBL/GenBank/DDBJ databases.		
CC	- - CAUTION: The sequence shown here is derived from an		
CC	EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which is		
CC	preliminary.		
DR	EMBL:CAA01014660; CAGC1841_1; -; Genomic_DNA.		
FT	NON_TER 1		
SQ	SEQUENCE 440 AA; A2DBB6C7CF9EB83099 CRC64;		
Query Match	71.9%; Score 1647; DB 2; Length 440;		
Best Local Similarity	67.9%; Pred. No. 8.4e-129;		
Matches	298; Conservative 47; Mismatches 62; Indels 32; Gaps 4;		
Oy	12	PNKEPVVKYKELVIVVYGAALPNQDGDKRKRSPFALKRKANGKVSKTRVISTPDKSAI	71
Oy	4	PKVKYKELVIVVYGAALPNQDGDKRKRSPFALKRKANGKVSKTRVISTPDKSAI	71
Db	72	SKCKQHQSISYTLSNQTVVETHDKDQMVGESTESIDFWTDTSGSQTNTDEAQI	131
Oy	64	PKVKYKELVIVVYGAALPNQDGDKRKRSPFALKRKANGKVSKTRVISTPDKSAI	63
Db	132	TQSTISRFACRIVCRNEPTARFAAGFSSKNTFLGERAKWNPDGNDGLTNGVL	191
Db	124	APSTISRFACRIVCRNEPTARFAAGFSSKNTFLGERAKWNPDGNDGLTNGVL	183
Oy	192	VMPRRGGTTESSQGWRETSVCGVTTBETRSAQQRGKV	--
Db	64	HSSQGHSISFTLSNQTVVETHDKDQMVGESTESIDFWTDTSGSQTNTDEAQI	123
QY			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].		
RC	TISSUE= Mammary tumor;		
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strasberg R.L., Fengold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schulter G.D.,		
RA	Altshul S.F., Zeeberg B., Butcko K.H., Schaefer C.F., Bhat N.K.,		
RA			
RT	Analyses of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs";		
RL	Nature 420:563-573(2002).		
RN	[2]		
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Db	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Oy	402	TQVNGEONCILKUFIQGPID	420
Db	423	AAI-GSPGWTLIFQGPID	440
Db	234	--ESEINVLQDGSLIDICGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	290
Oy	243	IQAEGTSALDGSILDCGATLMLTADGEFLTPQKHAEALRQEINAARQCPVGLNT	302
Db	291	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	341
Oy	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Db	342	GPyVPWLGCAGFVYDAGPPTAFCGHCAGSEKSAYMSQIPRHGTHAFAACPCFCA	401
Oy	363	GPyVPWLGCAGPVMNDAGPATPHEVPCGHYSERT"KWAATPLPHGTHAFAACPCFCS	422
Db	402	TQVNGEONCILKUFIQGPID	420
Oy	423	AAI-GSPGWTLIFQGPID	440
Db	303	IAPSPSLRKVEEKOPWAYISCGHVGHGHRSDTE-----ANERBCPMRTV	362
Oy	342	GPyVPWLGCAGFVYDAGPPT	



RA	Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E.,	FT	VARSPLIC	52	75	Missing (in isoform 2).
RA	Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,	FT				/FTId=VSP 008640.
RA	Raha S.S., Loqueilano N.A., Peters R.D., Mulay S.J.,	FT	VARSPLIC	282	331	ENESNVQDGSLIDLGATLWRTPLAFTKOLEAQ
RA	Bosak S.A., McEwan P.J., McKean K.J., Malek J.A., Gunaratne P.H.,	FT				OBANARQ->GGIISPPSLPQPHKUPLPLPGDDL
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	FT				OSFCPRQQARYQGIPGGGS (in isoform 4).
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	FT				Missing (In isoform 4).
RA	Fahey J., Melton B., Ketteman M., Madan A., Rodriges S., Sanchez A.,	FT				/FTId=VSP 008642.
RA	Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.S.,	FT				H -> L (in Ref. 3).
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,	FT				H -> L (in Ref. 3).
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	FT				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,	FT				
RA	Schneller A., Schein J.R., Jones S.J.M., Marra M.A.,	FT				
RT	"Generation and initial analysis of more than 15,000 full-length human	FT				
RT	and mouse cDNA sequences.";	RL				
CC	Proc. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RL				
CC	-!- FUNCTION: Scaffold protein which probably links Toll-like	CC				
CC	receptors (TIRs) to basic cellular processes via its intractivation	CC				
CC	with the complex containing TRAF6, IRAK1, MAP3K14 and MAP3K7.	CC				
CC	-!- INTERACTION:	CC				
PS1617-IRAK1; NbExp=1; Intact=EBI-448457, EBI-358664;	PS1617-IRAK1; NbExp=1; Intact=EBI-448466, EBI-358664;	DB				
Q99558-MAP3K14; NbExp=1; Intact=EBI-448472, EBI-358664;	Q99558-MAP3K14; NbExp=1; Intact=EBI-448472, EBI-358664;	QY				
Q99558-MAP3K14; NbExp=1; Intact=EBI-448466, EBI-358664;	Q99558-MAP3K14; NbExp=1; Intact=EBI-448466, EBI-358664;	DB				
Q99558-MAP3K14; NbExp=1; Intact=EBI-448457, EBI-358611;	Q99558-MAP3K14; NbExp=1; Intact=EBI-448457, EBI-358611;	QY				
Q93318-MAP3K7; NbExp=1; Intact=EBI-448457, EBI-358684;	Q93318-MAP3K7; NbExp=1; Intact=EBI-448466, EBI-358684;	DB				
Q93318-MAP3K7; NbExp=1; Intact=EBI-448472, EBI-358684;	Q93318-MAP3K7; NbExp=1; Intact=EBI-448472, EBI-358684;	QY				
Q9Y4K3; TRAF6; NbExp=1; Intact=EBI-448472, EBI-359276;	Q9Y4K3; TRAF6; NbExp=1; Intact=EBI-448466, EBI-359276;	DB				
Q9Y4K3; TRAF6; NbExp=1; Intact=EBI-448457, EBI-359276;	Q9Y4K3; TRAF6; NbExp=1; Intact=EBI-448457, EBI-359276;	QY				
-!- ALTERNATIVE PRODUCTS:	-!- ALTERNATIVE PRODUCTS:	DB				
Event=Alternative splicing; Named isoforms=4;	Event=Alternative splicing; Named isoforms=4;	QY				
CC	Name=1; Synonyms=Alpha_A;	CC				
CC	IsoId=Q8N2H9-1; Sequence=Displayed;	CC				
CC	Name=2; Synonyms=Beta_B;	CC				
CC	IsoId=Q8N2H9-2; Sequence=vsp_008640;	CC				
CC	Name=3;	CC				
CC	IsoId=Q8N2H9-3; Sequence=vsp_008639;	CC				
CC	Note=No experimental confirmation available;	CC				
CC	Name=4;	CC				
CC	IsoId=Q8N2H9-4; Sequence=vsp_008641, vsp_008642;	CC				
CC	Note=No experimental confirmation available;	CC				
CC	-!- TISSUE SPECIFICITY: Highly expressed in brain, heart and testis,	CC				
CC	and at lower level in kidney, liver, lung, placenta, small	CC				
CC	intestine, spleen and stomach. Isoform 1 is not expressed in lung.	CC				
CC	-!- SIMILARITY: Belongs to the Pellino family.	CC				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration	CC				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	CC				
CC	the European Bioinformatics Institute. There are no restrictions on its	CC				
CC	use as long as its content is in no way modified and this statement is not	CC				
CC	removed.	CC				
DR	EMBL: AF48456; AA041465.1; -; mRNA.	DB				
DR	EMBL: AF48457; AA041466.1; -; mRNA.	DB				
DR	EMBL: AL834395; CAD39057.1; -; mRNA.	DB				
DR	EMBL: AK072201; BAB85015.1; -; mRNA.	DB				
DR	EMBL: AK072253; BAC1499.1; ALT INIT; mRNA.	DB				
DR	EMBL: AK094060; BAC04275.1; -; mRNA.	DB				
DR	EMBL: BC021256; AAH21256.1; -; mRNA.	DB				
DR	EMBL: BC025723; AAH25723.1; -; mRNA.	DB				
DR	INTACT; Q8N2H9; -.	DB				
DR	Ensembl; ENSG0000174516; Homo sapiens.	DB				
DR	InterPro; IPR006000; Pellino.	DB				
DR	PANTHER; PTHR12008; Pellino; 1.	DB				
DR	Pfam; PF04710; Pellino; 1.	DB				
KW	Alternative Splicing	DB				
PT	VARSPLIC 48 110 Missing (in isoform 3).	DB				

Search completed: March 1, 2006, 21:00:02  
Job time : 235 secs

GenCore version 5.1.7  
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## OM protein - protein search, using SW model

Run on:

March 1, 2006, 20:56:21 ; search time 40 seconds

(without alignments)

1010.276 Million cell updates/sec

Title: US-10-041-030-4  
 Perfect score: 2290  
 Sequence: 1 MFSPGQBEHCAPNPKPVKG.....ATOLVGEONCNIKLIFQGPID 420

## Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80;\*

pir1;\*

pir2;\*

pir3;\*

pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result

No.

Score

Match

Length

DB

ID

## Description

Query	Match	Length	DB	ID	Score	No.
						*
1 890	38.9	484	2	T25731		1
2 122.5	5.3	215	2	T28405		2
3 103.5	4.5	1591	2	A54146		3
4 100	4.4	350	1	T03447		4
5 98	4.3	994	2	A10072		5
6 95.5	4.2	978	2	C85647		6
7 95.5	4.2	978	2	B81593		7
8 95	4.2	978	2	G72076		8
9 92.5	4.0	874	2	C8804		9
10 92	4.0	3051	2	S42373		10
11 91.5	4.0	476	2	T40746		11
12 91.5	4.0	1449	2	A12017		12
13 90.5	4.0	520	2	B39330		13
14 90	4.0	823	2	F90314		14
15 90	3.9	449	1	NBDHHS		15
16 90	3.9	449	1	S41947		16
17 90	3.9	1119	2	A88481		17
18 90	3.9	1231	1	NBRHH		18
19 90	3.9	1986	2	F71405		19
20 89.5	3.9	823	2	G9048		20
21 89.5	3.9	823	2	E8706		21
22 89	3.9	298	1	A10942		22
23 89	3.9	681	2	AD3318		23
24 89	3.9	747	2	T36812		24
25 89	3.9	2098	2	T13166		25
26 89	3.9	2265	1	FNB		26
27 89	3.9	2458	2	T1720		27
28 89	3.9	2660	2	E8582		28
29 88.5	3.9	558	2	T02704		29

## ALIGNMENTS

RESULT 1  
 T25731  
 hypothetical protein F25B4.2 - *Caenorhabditis elegans*  
 CSpecies: *Caenorhabditis elegans*  
 CDate: 15-Oct-1999 #sequence\_revision 14 Oct-1999 #text\_change 31-Dec-2004  
 CAccesion: T25731  
 R.Gattung, S.  
 Submitted to the EMBL Data Library, July 1996

A>Description: The sequence of *C. elegans* cosmid F25B4.

A&gt;Reference number: 224076

A&gt;Accession: T25731

A&gt;Status: Preliminary; translated from GB/EMBL/DDJB

A&gt;Molecule type: DNA

A&gt;Residue: 1-484 &lt;GAT&gt;

A&gt;Cross-references: UNIPROT:Q29967; UNIPARC:UPI000179271; EMBL:U64842; PIDN:AAB37081.1;

A&gt;Experimental source: strain Bristol N2; clone F25B4

A&gt;Gene: CESP:F25B4.2

A&gt;Map position: 5

A&gt;Introns: 35/2; 78/3; 112/3; 136/1; 191/3; 334/3; 406/2; 437/3

Query

Match

Length

DB

ID

Best Local Similarity 38.9%; Score 890; DB 2; length 484;

Matches 178; Conservative 43.5%; Pred. No. 1-7e-64; Mismatches 143; Indels 20; Gaps 7;

Ov 19 YAKLWLVGNGALPNQDGRGR-KSRFLAYKPKANGVKPSVTWVHSPQSKAISCKQH 77

Db 28 YEBILILGGNGQENRATMSKRYLTQKTVRNDRD-SANGIKCTVHNVSID-TKLTKOARH 86

Ov 78 SISYTLSRNQNTVVEYTHKDQMFGQRSSTESPSPIDPVYDT-ISSQNTDE---QI 131

Db 87 TVSFPHSDPSNKSVTYEYADPSKDMFOIGRASDDOIDPTVTDIWTMELPERSHDAAVARPQI 146

Ov 132 -----TQSTISRFACRIVCNEPYTARTFAAGEDDSKQFLIGKAKWNPKDGDNG 184

Db 147 DVLKEKGDTTSRISRFACRLIDRENNSKAYUYAGFDHQHNSINKSLKWKNSHEVD 206

Ov 185 LTINGVUWMPHRG---GFTTESOPGWRETSVCGVYVLTETRSAQORGKLVESPTNV 240

Db 207 LTTNGVUWMPKDDLDLTDVVKPMWKRREVISINGDVPEPRVTRSSAKGVFPWENTML 266

Ov 241 QDPSLIMCGATLWRPAGLFLHTPQKHLARQESINAARQCPVGLNTLAPSINKE 300

Db 267 QDPLLIDCGATLWRPAGLFLHTPQKHLARQESINAARQCPVGLNTLAPSINKE 326

Ov 301 VWEKQWAVLSCGHVYGHWHGRSDTEANBERCECMCRTVGP-YVPLWLGCBAFYVDA 359

Db 327 QINRRQFVYLQOGHVGGRHVGVOENSGQSGKCFICLVESETIVQLSMGMEPSHIDS 386

Ov 360 GPFTHAFTPGCIVGCSERAKTWSOIPLPHGTHAHPACPGCATOLVGEQ 408

Db 387 GVLDHFTNPCCGHMASKQVLYWSRIPPLQGICRYDPWCPFCYOLLATER 435

transcription fact  
 hypothetical prote  
 hypothetical prote  
 probable oxidoredu  
 krueppel-type zinc  
 nitrogenase (EC 1)  
 hypothetical prote  
 probable salt-indu  
 hypothetical prote  
 peroxidain - farn  
 multifunctional am

RESULT 2

T28405 hypothetical protein - *Melanoplus sanguinipes* entomopoxvirus

C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 09-Jul-2004

C;Accession: T28405

R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.

J;Virol. 73, 533-552, 1999

A;Title: The genome of *Melanoplus sanguinipes* entomopoxvirus.

A;Reference number: Z20484; MUID:919102612; PMID:9847359

A;Accession: T28405

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-215 <AFO>

A;Cross-references: UNIPROT:Q9YVJ8; UNIPARC:UPI00000F81BF; EMBL:AF063866; NID:94049647; C;Genetics;

A;Note: MSV244

Query Match 5.3%; Score 122.5; DB 2; Length 215;

Best Local Similarity 18.7%; Pred. No. 0.016; Mismatches 84; Indels 151; Gaps 13;

Matches 61; Conservative 31; MisMatched 84; Indels 151; Gaps 13;

Qy 81 YTLRSRNQTVWVYHDKDPTDMFQGRSDESPIDFWTTISGQNTDBAQITSIHPA 140

Db 19 YNLINYNK----NYT-----FTIGRN--SKCDIFIND-----KKISNTA 50

Qy 141 CRIVCDRVEPYTAKIFAAFGFDSSKNIFGEKAQKWNKNPQDHMDGLITNGVLVMPRGFT 200

Db 51 CIKCD-YEKKCCTIYGGCSNSKCVLYFDNN-----DQILQNGIFPKFPN--- 94

Qy 201 ESEOPGVREIISVGVDVYLTETRSAQORGKLVESETNTVQDQDSLIDLGATLWRADG 260

Db 95 -----LEWDLSINGNIVYL-----RSNIKLNLINEBLDTFLIDISGNIVIWRST-- 139

Qy 261 LHRHPTQKIEALRQEINAPRQCPGVLNTAFLPSINRKEVVERKQPAWYLSCHVHG 320

Db 140 ----- 139

Qy 321 NWGHRSRDSSTEANERCC--PMCRTCVPYVPLWLGCAGFYVDAQPEHTAFTPCCGIVCSEKSA 378

Db 140 -----EYMFVKCGHKINKKTA 174

Qy 379 KYNSQL-----PLPHGTHAFAACPF 400

Db 175 TFWKKTOKLCNDIYTNYKLYKLICCPFC 201

RESULT 3

A54146 invasion-inducing protein, Tiam-1 - mouse

C;Species: *Mus musculus* (house mouse)

C;Date: 02-Aug-1994 #sequence\_revision 02-Aug-1994 #text\_change 09-Jul-2004

C;Accession: A54146

R;Habets, G.G.M.; Scholtees, E.H.M.; Zuydgeest, D.; van der Kammen, R.A.; Stam, J.C.; Berellin, 53-549, 1994

A;Title: Identification of an invasion-inducing gene, Tiam-1, that encodes a protein with

A;Reference number: A54146; MUID:94243921; PMID:7999144

A;Accession: A54146

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1591 <HAB>

A;Cross-references: UNIPROT:Q60610; UNIPARC:UPI0000028180; GB:U05245; NID:9497638; PID: P1040-1234/Domain: CDC24 homology <CD24>

Query Match 4.5%; Score 103.5; DB 2; Length 1591;

Best Local Similarity 22.1%; Pred. No. 8.7; Mismatches 81; Conservative 53; MisMatched 166; Indels 67; Gaps 18;

Matches 81; Conservative 53; MisMatched 166; Indels 67; Gaps 18;

Qy 3 SPGOBEHCAPNKEPVKGVLVLYGNGALPNQDRGRKSRAFLYKRPKANGVKPSTHVI 62

Db 219 SPROLSTC---QRANSLGDIYAQKNSGVKG---PRNPFSSYCRNLVSDIDPLAKHM 272

Qy 63 -----SPQAS--KAISCKGHSISYTLSRNQTV--VEYTHDKDPTDMFQVGRSTE-- 109

Db 273 PPAABEEPPYSINTLCLKSHCLSGATINQISLSSMOGRAKTIQDNTGEGSFA 332

Qy 110 -SPIDFVVTPTSGSQWMDAIIQTOSISRACTIVCDDNEYTAIRFAGFDSSENIFL 168

Db 333 DSIEGATTDTDLISRNS--ATNSYS-----PPTGRAF-VESDGSST 375

Qy 169 GEGAK--WKNPQDHMDGLITNGVLVMPRGFT---SQPGWRETSVCGDVTL 220

Db 376 GDAROGTYENFRELNSTMSLHEAGSAHSFQSGRSLSP--QSDILITAQGT 434

Qy 221 RETRS-----AQQRGLVSEBTNVQDGSLLDCGATLWRTAD--GLFHTPTQKHI 270

Db 435 RKAGALAVKFLVHKKOKKVESATRKWKHYWVLSKCTTFFETDGRSGIDHNSVPKHA 494

Qy 271 FAHQETNAPIARQCPG-----LNTLAFFSINRKEVVERKQPAWYLSCHVHG 321

Db 495 VVVENSTVQAVPFBPKKDPFVFLSNSLGDADFQTSQTELENWITAIHSACAABARRH 554

Qy 322 WGRHSDT 328

Db 555 --HKBDT 559

RESULT 4

T3447 dihydrokaempferol 4-reductase (EC 1.1.1.219) A - sorghum

C;Species: *Sorghum bicolor* (bicolor)

N;Alternate names: dihydroflavonol 4-reductase; NADPH-dependent reductase A1-a

C;Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004

R;Chen, M.; Sanchez, P.; Bennetzen, J.L.

A;Title: Sequence organization and conservation of Sh2/A1-homologous regions of sorghum ε Genes 143, 435-443; 1998

A;Reference number: Z14952; MUID:98133900; PMID:9475753

A;Accession: T03447

A;Status: preliminary; translated from GB/EMBL/DDJB

A;Molecule type: DNA

A;Residues: 1-350 <CHB>

A;Cross-references: UNIPROT:P93776; UNIPARC:UPI00000A710A; EMBL:AF010283; NID:92735839; I

A;introns: 52/1; 108/3; 173/3

C;Superfamily: dihydrokaempferol 4-reductase

C;Keywords: oxidoreductase

Query Match Best Local Similarity 4.4%; Score 100; DB 1; Length 350;

Matches 47; Conservative 21; MisMatched 71; Indels 56; Gaps 9;

Qy 169 LGEKAAKTKNPQHMDGLITNGVLVMPRGFTESQPGWREISVCGDVTLRERSAQ 227

Db 1 MGEVWATEATG-----GAGVKVPPVYGAFL-----GSMVUMKLIQQGTVTR----- 48

Qy 228 ORGKLVVESBTNVQDGSLLDCGAT--LLW-----RTADGFHTPQKHI 270

Db 49 -----VDPANVVKTKLIDLGATERSLNGADLADEGSFDAIRGCTGVFHATPMDF 103

Qy 271 BALRQEINAPR-----OCPVG--LNTLAFFSINRKEVVERKQPAWYLSCHVHG 318

Db 104 ESKDOPENEVKIFTVEGMMSIMRACKAEAGTVRRIVFISAGTVNIEERQ-----RPVYD 156

Qy 319 NWGHRSRDSSTEANER 333

Db 157 QDW-----SDVDFCQR 168

RESULT 5

A10072 probable autotransporter protein YPO0587 [imported] - *Yersinia pestis* (strain C092)

C;Species: *Yersinia pestis*

C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004

C;Accession: AI0072  
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
den-Terraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
Nature 413, 523-527, 2001  
A;Title: Genome sequence of *Versinia pestis*, the causative agent of plague.  
A;Reference number: AB0001; MUID:21470413; PMID:11586360  
A;Accession: AI0072  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-994 <KUR>  
A;Cross-references: UNIPROT:Q9P286; UNIPARC:UPI00000DC570; GB:AL590842; PIDN:CA09444\_1;  
C;Gene: YPO0587

Query Match 4.3%; Score 98; DB 2; Length 994;  
Best Local Similarity 22.2%; Pred. No. 13; Mismatches 70; Conservative 53; Indels 139; Gaps 17;  
Matches 27; Status: preliminary

Qy 13 NKEPVK--YGBLWVLGNGALNGD-RGRRSKRSPALYKRPKA-NGVKPSTHVISPOA 67  
Db 27 NSPIATCVAALIFIGSSVVIANPDHEGIVVKGSKLNKQSAVNAIINEGNSIVLDSA 86

Qy 68 SKAISCKQHSISYTSILSNQTVWVYHDKTUMQGRSRSIDPFDVUTDTSQS-QN 125  
Db 87 SAHHTAVNTGSI-FTLKEDSDTADIT--SVTGFPSFLSGSSTKANINTV---LSCGMILEV 138

Qy 126 TDPAQTOSTISRFACRIVCDRNEPYTARIAFFAGFDSSRNTEFGEKAARKWQDGHMD-- 183  
Db 139 NDASASITTTIS-----SDIEKKSTRLYQD--SAKTTWGDINGLIVUSGSRAET 189

Qy 184 GLUTTINGVLMVMHPRGGPTERSQEWRETLVCGVDTYRERTRAAQQRGKLVESERTVNLQDG 243  
Db 190 HVRTRGKGKLUVY----SESEQPTLNTQIAQSTL-TLKSDDVTELEGKTFVSSSAT-IKTTG 241

Qy 244 SLDLGCATLMLRTADGEHTPKXHMEURQNSINARPPQCGVQNLAPPNSIRKVE 303  
Db 242 HLLDNQGL-----IFNSKDIDVIERAMIDQGSLSLTKENP--LTTLTLSSAG---- 285

Qy 304 EKOPFW-AYLSCCHVH 317  
Db 286 - DAWWVSYVVSQETH 299

RESULT 6

C86547 Polymorphic outer membrane protein H family [imported] - Chlamydophila pneumoniae (strain C; Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Accession: C86547  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (strain C; Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C;Gene: C86547  
C;Experimental source: strain J138  
C;Superfamily: Polymorphic membrane protein H family

A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A;Reference number: AB6491; MUID:20330349; PMID:10871362  
A;Accession: C86547  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-978 <STO>  
A;Cross-references: UNIPROT:Q9ZB95; UNIPARC:UPI0000131C83; GB:BA000008; NID:98978825; PI

Qy 102 PQWRSTESPIDRVTDITSGSQTDEAQTOQTISRFACRIVCDRNE----- 149  
Db 523 FTIGKLAFLDPFSFLKRDVSASVNSVAGTKNVI----LIGALVLDHNDVTLDYMSLQS 576

Qy 150 PYTARIAGAAGPSKSKNTELEGRAKKWNPDGMDGJTG-----VLMHPRG 197  
Db 577 PVAIPI-----AVFKGATWTKQFPDGEIATPSHYGYQCKWSVTSRPLPILAPDG 627

Qy 198 GFTEESQP-----GVREBISVGDVITLRETRSAQQRGKLVES-----TNVL 240  
Db 628 GRGGPRPSANTLYAVNSDITVRSVIL---DPERYGEVVSNSWISLGNQAFSDIL 683

Qy 241 QDPSLIMQGATLWLRDGL---FHTPTOKR 269  
Db 684 QDVLIDHPIGLSI---TAKALGAYVETPROCH 713

RESULT 8

C72076 Polymorphic outer membrane protein h family - Chlamydophila pneumoniae (strain CWL029)  
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: G72076  
R;Kalmen, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A;Title: Comparative Genomes of *Chlamydia pneumoniae* and *C. trachomatis*.  
A;Reference number: A72000; MUID:99206606; PMID:10192388  
A;Accession: G72076  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-978 <ARN>  
A;Cross-references: UNIPROT:Q9ZB95; UNIPARC:UPI000046ABB; GB:AE001629; GB:AE001363; NID:  
A;Experimental source: strain CWL029  
C;Genetics:  
A;Gene: Pmp\_14  
C;Superfamily: Polymorphic membrane protein H family

DB 577 PVAIPI-----AVFKGATWTKQFPDGEIATPSHYGYQCKWSVTSRPLPILAPDG 627  
Qy 198 GTTBESQP-----GVWRBISVGDVITLRETRSAQQRGKLVES-----TNVL 240  
DB 628 GPGGPBPSSANTLYAVNSDITVRSVIL---DPERYGEVVSNSWISLGNQAFSDIL 683  
Qy 241 QDPSLIMQGATLWLRDGL---FHTPTOKR 269  
DB 684 QDVLIDHPIGLSI---TAKALGAYVETPROCH 713

RESULT 7

B81593 Polymorphic membrane protein H family CP0298 [imported] - Chlamydophila pneumoniae (strain C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae  
C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004  
C;Accession: B81593  
R;Read, T.D.; Brunham, R.C.; Sheen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, R.; C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, N.; Nucleic Acids Res. 28, 1397-1406, 2000  
A;Title: Genome Sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.  
A;Reference number: A81500; MUID:20150255; PMID:10684935  
A;Accession: B81593  
A;Residues: 1-978 <REB>  
A;Molecule type: DNA  
A;Cross-references: UNIPROT:Q9ZB95; UNIPARC:UPI0000131C83; GB:AE002191; GB:AE002161; NID  
A;Gene: CP0298  
C;Superfamily: Polymorphic membrane protein H family

Query Match 4.2%; Score 95.5; DB 2; Length 978;  
Best Local Similarity 22.1%; Pred. No. 20; Mismatches 47; Conservative 25; Indels 74; Gaps 67; Gaps 9;  
Matches 47; Status: preliminary

Qy 102 PFGVRSRSPIDPVUTPVTISQNTDEAQTOQTISRFACRIVCDRNE----- 149  
Db 523 FTIGKLAFLDPFSFLKRDVSASVNSVAGTKNVI----LIGALVLDHNDVTLDYMSLQS 576

Qy 150 PYTARIAGAAGPSKSKNTELEGRAKKWNPDGMDGJTG-----VLMHPRG 197  
Db 577 PVAIPI-----AVFKGATWTKQFPDGEIATPSHYGYQCKWSVTSRPLPILAPDG 627

Qy 198 GFTEESQP-----GVREBISVGDVITLRETRSAQQRGKLVES-----TNVL 240  
Db 628 GRGGPRPSANTLYAVNSDITVRSVIL---DPERYGEVVSNSWISLGNQAFSDIL 683

Qy 241 QDPSLIMQGATLWLRDGL---FHTPTOKR 269  
Db 684 QDVLIDHPIGLSI---TAKALGAYVETPROCH 713

Query Match 4.2%; Score 95.5; DB 2; Length 978;  
 Best Local Similarity 22.1%; Pred. No. 20; Gaps 9;  
 Matches 47; Conservative 25; Mismatches 74; Indels 67;

Qy 102 FQYGRSRSTESPINWPTDITSGSNTDEAQITOSTISRFACRIVCDRNE----- 149  
 Db 523 FTIGKLAEDPFSSLKRDPSVSAVNAGTKNVT-----LTGALVLDEHDVTDLYDMVSLQS 576

Qy 150 PYTARIFAFGPISSKNIFLGEKAQKWNPDGMGDLT-----VLMWPRG 197  
 Db 577 PYAIP-----AVFGATVTKCPRPDGFATPNSYGYCKWSYTWSRPLLIPADG 627

Qy 198 GFTFEESQP-----GVREIISVGDVVTLRETSQAQQGKLVESE-----TNVL 240  
 Db 628 GFGGGPSPSANTIVAVWNSDTLVSTVIL--DPERYGETVSLSLWISFLGNOAFSDIL 683

Qy 241 QPSLSDLGATIWLWTRDGL---FMPPTQKH 269  
 Db 684 QPVLLIDRPGLSI---TAKALGAYVETPROQH 713

RESULT 9

alanine-tRNA ligase (EC 6.1.1.7) NM1788 [imported] - *Neisseria meningitidis* (strain 224  
 C;Species: *Neisseria meningitidis*  
 C;Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
 C;Accession: CB8104  
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, S.; Holroyde, S.; Jolley, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
 A;Reference number: A81775; MVID:20222556; PMID:10761919  
 A;Accession: CB8104  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-874 <PAR>  
 A;Cross-references: UNIPROT:Q9JTC4; UNIPARC:UPI0000136315; GB:AL162757; GB:AL157959; NID  
 A;Experimental source: serogroup A, strain Z2491  
 C;Genetics:  
 C;Gene: alsB; NM1788  
 C;Superfamily: alanine-tRNA ligase  
 C;Keywords: ligase

Query Match 4.0%; Score 92; DB 2; Length 3051;  
 Best Local Similarity 21.6%; Pred. No. 1.8e+02; Gaps 156; Matches 94; Conservative 44; Mismatches 156; Indels 142; Gaps 24; Matches 94;

Qy 4 P5G-----EEHCAPNPK-----EP-----VKYGEELVLTGYNALPGDRGRKSRLA YKR 48  
 Db 1687 PGKVCSAPEVPPNHDCCSAAVCEPLGGKIQCVCIQGYWDQSPGSQKGRVCVRNNACHD 1746

Qy 49 PRXANGVLFESTVHVISTPQASKAISCKQHQSISYTLURNOTVWVYTH-DKOTDMFQYRS 107  
 Db 1747 PRUN-----TC-SRA, CYDERBRGYZRCBKRCFMDSPPDSSORGRV 1786

Qy 108 TESP-----IDFVUTDTISGSNTDEAQITOSTISRFACRIVCDRNE 149  
 Db 1787 CIRPPPSPPPRHPQCDPERUDCHPAGTCRATGAQ-----YTCBCLSGYUDSPRPNK 1841

Qy 150 PYTARIFAFGPISSKNIFLGEKAQKWNPDGMGDLT--VLMWPRG 203  
 Db 1842 PGRLCVLTFPVCLDPEON-----DCHAIAICSEVNGPEKTYCKCRDGTYDES 1888

Qy 204 QPSWVREISVSCDVVYTLRETSQAQQGKLVESETNLQDLSLIDC-----GATLWRTA 258  
 Db 1889 PDPLRRGRIC-----KOLINICLDRSLANDCHSLAVERKDLPNGY----- 1928

Qy 259 DGLFHTPKHTEALRQEINAARPO--CPVGLNTLAPSINR---KEVVEEKQPMAYLS 312  
 Db 1929 -----CQCQCPINAKQDPSDPKPRGRICSLSNECANPSLNSCAFADCFEDEENGY--R 1978

Qy 313 CGTVHGKTH-----NWGHRSIDTEANE-----RBCCPMCTVGVYVPLMGCEAGFYV 357  
 Db 1979 CCRNGHFDPPAHPGHRCFSMINECDSSNLNDCDRNANCIDTAGGYD--CACKAP-YR 2034

Qy 358 DAGPPTTAFTPGHVC 373  
 Db 2035 DSCPPQ--SP-GRIC 2046

RESULT 11

T0476  
 Query Match 4.2%; Score 95.5; DB 2; Length 978;  
 Best Local Similarity 22.1%; Pred. No. 20; Gaps 9;  
 Matches 47; Conservative 25; Mismatches 74; Indels 67;

Db 556 NANMRNHSATHLMEKALDVLGGHVE--QKSLVNTABESTRFDISHPOAVTBAAEVER 612

Qy 203 -SQPGWHRBISVGDVYTLRETSQAQGKGKV-----ESETWVQPSL-IDLGGATL 254  
 Db 613 RVNEAVLNAVVAVNAIMMED--AOKTGAMMLPGEKYGEVRLQMGCFSTBLGGTHV 669

Qy 255 WRTAD-GIPTPTKHEALRQEINAARPOCPVGLNTLAPPSPNKEVE-----E 304  
 Db 670 SRVGDIGLFKLISEGGIIAGVRRIEAI----TGLNALKWAQOQERLVKDI LAETKQTE 724

Qy 305 KQWAVLSCGHW 317  
 Db 725 KDVLAQIAQGAH 737

C;Superfamily: translation initiation factor eIF-2A	
Query Match 4.0%; Score 91.5; DB 2; Length 576;	
Best Local Similarity 20.6%; Pred. No. 20; Matches 56; Conservative 35; Mismatches 98; Indels 83; Gaps 12;	Best Local Similarity 21.2%; Pred. No. 40; Matches 77; Conservative 39; Mismatches 126; Indels 121; Gaps 20;
QY 39 RKSRRPALKRKPKANGV-----KPSTWVVISPTQASKAISCKQHSITSYTLQRNQTV 90 3 QKSGFA-TRSKSLGLUNASENYASPKPKEAISEBARNATYSPNCK----- 47	QY 10 CA---PNEKPKVKGELVLGNGALPNDGRGRKSRP---AIVKRPKANGVKEPKSTVHVI 64
Db 91 VEYTHDKDTDMFQVGRSTSPIDPVFTDITISGSNTDEAQITQSTISRFACRIVCDRNEP 150 48 -----LFAVATATO-----VVINDTEG-----AKTGTLP----- 72	Db 7 DRAPIPDQAEKREGAVAVA-TAIEAGDERARAKFHWOFFEHYPAQDC----- 54
QY 151 YTARIPIAGFDSSKNIFLGAARKKVNPDCHMDGTTGVLUMHRRG-----FTEESQP 205 73 -AANTYELGFSRSP-----LSGYLTSTWRPSKEADGPKONKHWMNTETGOLVFSFVORNQ 126	QY 206 GVRREBISVCGDVYVTRETSAQQRQLVKESETENVQDGSLIDLCCATLJURTAGDLHTP 265 127 G-WHL-----QYTCDESLA--RLVTEVHPTGTMNSKGPIAKURVEGISDPALSP 175
Db 266 TORKHEALRQEINARAPQCPVGLNTLAFPSIN 297 QY 176 GONEHAVAV---FIPERKKGAPASVRYTISIPEFN 204	Db 291 LAFPSINRKVEYKEOPWAVYSCGEHWGY 319 Db 299 LSVYRVSK--VIEELP----NCQLINGY 320
RESULT 12	
A12017 Hypothetical protein al11695 [imported] - Nostoc sp. (strain PCC 7120)	QY 94 THDKDTDMFQVGRSTSPIDPVFTDITISGSNTDEAQITQSTISRFACRIVCDRNEP--- 150
C;Species: Nostoc sp. PCC 7120	Db 277 TYDREKGLWEKQKISBQ-----DYLISARMLQEAQISVNAQQLTAIGASNSSTALN 329
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120	QY 151 YTARIPIAGFDSSKNIFLGAARKKVNPDCHMDGTTGVLUMHRRG-----FTEESQP 209
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004	Db 330 RYELRAFPAGMIVKEHSLGAEVADANV-----FTEISDLSSWVA 369
C;Accession: A12017	QY 210 EISVCG-DVITLR-EIRSQORGKVKESETENVQDGSLI-----IDLGATLW 255
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Yamada, M.; Iriuchi, S.; Nakazaki, N.; Shinjo, S.; Sugimoto, M.; Takazawa, M.; Yabuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001	Db 370 EFPVSAKDVVERVIRIGKASTNSASSVTKADTIVTGVSLIGEQTRTAKARTLTNPQMAW 429
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120	QY 256 RTADGHLFHTPTQKHEALRQEINARAPQCPVGLNTLAFPSINRKVEW 302
A;Reference number: AB1807; MVID:21595285; PMID:11759840	Db 430 R-PGLFVT-----VDFVGDADVVPVAVKTEAVQDVNGESTV 464
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-1449 <KUR>	
A;Cross-references: UNIPROT:Q8YWC0; UNIPARC:UPI00000CB194; GB:BA000019; PIDN:BAB78061.1; A;Experimental source: strain PCC 7120	
A;Gene: al11695	
RESULT 13	
Query Match 4.0%; Score 90.5; DB 2; Length 520;	Query Match 4.0%; Score 90.5; DB 2; Length 520;
Best Local Similarity 23.3%; Pred. No. 21; Mismatches 94; Indels 57; Gaps 8;	Best Local Similarity 23.3%; Pred. No. 21; Mismatches 94; Indels 57; Gaps 8;
Matches 53; Conservative 23; Mismatches 94; Indels 57; Gaps 8;	Matches 53; Conservative 23; Mismatches 94; Indels 57; Gaps 8;
QY 94 THDKDTDMFQVGRSTSPIDPVFTDITISGSNTDEAQITQSTISRFACRIVCDRNEP--- 150	QY 94 THDKDTDMFQVGRSTSPIDPVFTDITISGSNTDEAQITQSTISRFACRIVCDRNEP--- 150
Db 277 TYDREKGLWEKQKISBQ-----DYLISARMLQEAQISVNAQQLTAIGASNSSTALN 329	Db 277 TYDREKGLWEKQKISBQ-----DYLISARMLQEAQISVNAQQLTAIGASNSSTALN 329
QY 151 YTARIPIAGFDSSKNIFLGAARKKVNPDCHMDGTTGVLUMHRRG-----FTEESQP 209	QY 151 YTARIPIAGFDSSKNIFLGAARKKVNPDCHMDGTTGVLUMHRRG-----FTEESQP 209
Db 330 RYELRAFPAGMIVKEHSLGAEVADANV-----FTEISDLSSWVA 369	Db 330 RYELRAFPAGMIVKEHSLGAEVADANV-----FTEISDLSSWVA 369
QY 210 EISVCG-DVITLR-EIRSQORGKVKESETENVQDGSLI-----IDLGATLW 255	QY 210 EISVCG-DVITLR-EIRSQORGKVKESETENVQDGSLI-----IDLGATLW 255
Db 370 EFPVSAKDVVERVIRIGKASTNSASSVTKADTIVTGVSLIGEQTRTAKARTLTNPQMAW 429	Db 370 EFPVSAKDVVERVIRIGKASTNSASSVTKADTIVTGVSLIGEQTRTAKARTLTNPQMAW 429
QY 256 RTADGHLFHTPTQKHEALRQEINARAPQCPVGLNTLAFPSINRKVEW 302	QY 256 RTADGHLFHTPTQKHEALRQEINARAPQCPVGLNTLAFPSINRKVEW 302
Db 430 R-PGLFVT-----VDFVGDADVVPVAVKTEAVQDVNGESTV 464	Db 430 R-PGLFVT-----VDFVGDADVVPVAVKTEAVQDVNGESTV 464
RESULT 14	
F90914 hypothetical protein ECA2286 [imported] - Escherichia coli (strain O157:H7, substrain F) [imported]	F90914 hypothetical protein ECA2286 [imported] - Escherichia coli (strain O157:H7, substrain F) [imported]
C;Species: Escherichia coli	C;Species: Escherichia coli
C;Date: 10-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004	C;Date: 10-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F90914	C;Accession: F90914
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; DNA Res. 8, 11-22, 2001	R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno	A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: AG9629; MVID:21156231; PMID:11258796	A;Reference number: AG9629; MVID:21156231; PMID:11258796
A;Status: preliminary	A;Status: preliminary
A;Molecule type: DNA	A;Molecule type: DNA
A;Residues: 1-823 <HAY>	A;Residues: 1-823 <HAY>
A;Cross-references: UNIPROT:Q0X280; UNIPARC:UPI00000D0TE; GB:BA000007; PIDN:BAB35709.1; A;Experimental source: strain O157:H7, substrain RIMD 0509952	A;Cross-references: UNIPROT:Q0X280; UNIPARC:UPI00000D0TE; GB:BA000007; PIDN:BAB35709.1; A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Genetics:	A;Genetics:
A;Gene: ECA2286	A;Gene: ECA2286
RESULT 15	
Query Match 4.0%; Score 90.5; DB 2; Length 823;	Query Match 4.0%; Score 90.5; DB 2; Length 823;
Best Local Similarity 21.2%; Pred. No. 40; Matches 77; Conservative 39; Mismatches 126; Indels 121; Gaps 20;	Best Local Similarity 21.2%; Pred. No. 40; Matches 77; Conservative 39; Mismatches 126; Indels 121; Gaps 20;
Db 188 GPKPKVCVBHRGVVFLVKVNTYANNSCDEVILQLSIAFDAEFTEWAALINGGLVMP 247	Db 188 GPKPKVCVBHRGVVFLVKVNTYANNSCDEVILQLSIAFDAEFTEWAALINGGLVMP 247
QY 237 TNV---IQL-GSLIDICGATLWTRDUGLFLHPTQO---KHEALRQEINARAPQCPVGLNTLAFPSINRKVEW 290	QY 10 CA---PNEKPKVKGELVLGNGALPNDGRGRKSRP---AIVKRPKANGVKEPKSTVHVI 64
Db 248 INISSLQEIIGMAKQHVHTLWTA-GLFNLNVEQIEHKSLRQIL-----AGDV 298	Db 7 DRAPIPDQAEKREGAVAVA-TAIEAGDERARAKFHWOFFEHYPAQDC----- 54

OY	65 PQISKAKSCKGQHISIYTISLRNQTVVVEYTHIKDTMFMQVGISTESTPLDVVTDTLSGQ 124	Biochem. J. 205, 285-293, 1982
Db	55 -AYKFLVEDKGIPRRA-----LDSDAETWQENRNDSEASASFVYETESDPM 102	A;Title: Purification and structural studies on the complement-system control protein beta
OY	125 NTDEAQITQTSTISRFACTIVCRVCDNEPYTARIAGFDSKNI-----FLGERAK 174	A;Reference number: A26505; MUID:83048213; PMID:6215918
Db	103 N-----VTFDNLAPEVQNAVAVKFDTICENTIVDMVISAQELQEDMAT 145	A;Accession: A26505
OY	175 WKNRGDH----MDGLTNGV--LVMPRGTEBSQPGV-WREISVCGDVTLRTRS 225	A;Molecule type: protein
Db	146 F---DGHIVEALAKNKPETVNMYPPEKLKLAIGWYTKCKPGAKMPEDQEMRJWKKRGE 202	A;Residues: 19-20, 'Q', 22-29, 'V', 31-33, 'Q', 35 <SIM>
OY	226 AQORGKLVESETAVLQDGLSLIDGATLWRTADGLFHTPTKRIEALRQEINARPOCP 285	A;Cross-references: UNIPARC:UPI000174255
Db	203 RKEAGKTY-----SVVQLARA-----RANGQHTENSTGKIN----P 234	R;Barlow, P.N.; Norman, D.G.; Steinbasser, A.; Horne, T.J.; Pearce, J.; Driscoll, P.C.; Biochemistry 31, 3626-3634, 1992
OY	286 VGLNTLARPSINRKEVWKRKQPW-----AY-----LSCGIVHGYHNNKWHRSDETEAN 331	A;Title: Solution structure of the fifth repeat of factor H: A second example of the complement structure
Db	235 V-----IAAHR---BYKQTWKTLDDELAYALWPGDVADGNIDGSTHRWA-KNEVIDN 283	A;Reference number: A44551; MUID:9232659; PMID:1533152
OY	332 ERB 334	A;Accession: S10479
Db	284 GRB 286	A;Contents: annotation: NMR structure determination, residues 264-292
<b>RESULT 15</b>		
NBTHHS	complement factor H precursor, short splice form [validated] - human	R;Kristensen, T.; Wetzel, R.A.; Tack, B.F.
C;Species: Homo sapiens (man)	complement factor H-related protein; complement protein H	J. Immunol. 136, 3407-3411, 1986
C;Date: 31-Dec-993 #Sequence revision 23-Feb-1996 #Text change 09-Jul-2004		A;Titile: Structural analysis of human complement protein H: homology with C4b binding protein
C;Accession: S30313; B60288; A28877; A61103; A26505; S10479		A;Reference number: S10479; MUID:86169701; PMID:2537845
R;Rippeche, J., Davy, A.J., Harris, T.J.R.; Sim, R.B.		A;Molecule type: mRNA
Biochem. J. 249, 593-602, 1988		A;Residues: 226-401, 'Y', 403-449 <KR>
A;Title: The complete amino acid sequence of human complement factor H.		A;Cross-references: UNIPARC:UPI00002A635; NID:9180472; PID:AA52013.1; PID:9180472
A;Reference number: S00254; MUID:88134059; PMID:2963625		C;Comment: Factor H has also been found bound to cell membranes in an unknown manner. How
A;Accession: S03013		C;Genetics: <HF1>
A;Molecule type: mRNA		A;Gene: GDB:HPL1; HF
A;Residues: 1-449 <RIP>		A;Cross-references: GDB:120041; OMIM:134370
A;Note: part of this sequence, including the amino end of the mature protein was confirmed		A;Map position: 1q32-1q32
A;Cross-references: UNIPARC:P08603; UNIPARC:UPI00002A635; EMBL:X07523; EMBL:Y00716; NID:9180472		C;Genetics: <HF2>
R;Estbauer, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.		A;Gene: GDB:HPL2; HF
Biochem. J. 21, 799-802, 1991		A;Cross-references: GDB:129095
A;Title: Human complement factor H: two factor H proteins are derived from alternatively spliced mRNAs		A;Map position: 1q32-1q32
A;Reference number: A60238; MUID:9184292; PMID:1826264		C;Function:
A;Accession: B60238		A;Note: the correspondence between the two loci and the sequences indicated is unclear; it is also unclear if the alternative complement pathway is encoded by the same gene.
A;Status: not compared with conceptual translation		A;Description: a cofactor in the inactivation of C3b by serine protease I; also increases alternative complement pathway
A;Molecule type: mRNA		A;Pathway: complement alternate pathway
A;Residues: 1-33-434-449 <EST>		A;Keywords: alternative splicing; complement alternate pathway; glycoprotein; plasma
A;Cross-references: UNIPARC:UPI0001742E8; UNIPARC:UPI0001742E9		F1-18/Domain: signal sequence #status predicted <SIG>
A;Note: only portions of this 1.8 kilobase mRNA were sequenced		F19-49/Domain: complement factor H repeat homology <FH01>
R;Schulz, T.P.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P.		F20-80/Domain: complement factor H repeat homology <FH02>
Biochem. J. 16, 1351-1355, 1986		F21-85/14/Domain: complement factor H repeat homology <FH03>
A;Title: Human complement factor H: isolation of cDNA clones and partial cDNA sequence		F210-262/Domain: complement factor H repeat homology <FH04>
A;Reference number: A27877; MUID:87054207; PMID:2946589		F246-248/Region: cell attachment (R-G-D) motif
A;Accession: A27877		F267-320/Domain: complement factor H repeat homology <FH05>
A;Molecule type: mRNA		F325-385/Domain: complement factor H repeat homology <FH06>
A;Residues: 111-55-401, 'Y', 403-449 <SCH>		F389-442/Domain: complement factor H repeat homology <FH07>
A;Cross-references: UNIPARC:UPI00016AA0E; GB:X04697; NID:931991; PID:NCAB41739.1; PRD:91805295; PMID:2445583		F21-66-88, 85-129, 114-141-146-192, 178-205, 210-251, 237-262, 267-309, 294-320, 325-374, 357.
A;Note: an additional nucleotide present within the codon for Glu 310 was thought to be		F217/Binding site: carbohydrate (kan) (covalent) #status absent
R;Schwaeble, W.; Zwirner, J.; Schulz, T.P.; Linke, R.P.; Dierich, M.P.; Weiss, E.H.		Query Match Score 90; DB 1; Length 449;
Biochem. J. 17, 1485-1489, 1987		Best Local Similarity 20.1%; Pred. No. 19; Mismatches 124; Indels 106; Gaps 15;
A;Title: Human complement factor H: expression of an additional truncated gene product		Matches 67; Conservative 37; Mismatches 124; Indels 106; Gaps 15;
A;Reference number: A61103; MUID:8805295; PMID:2445583		QY 117 TPIISQNTDQAQITQTSTISRFACTIVCRVCDNEPYTARIAGFDSKNIIFGEKAKW- 175
A;Accession: A61103		D0 30 TEIITGSMS---DQTYPRGTQAIYKCR---PGYRSUQNVCRKGWV 72
A;Status: not compared with conceptual translation		OY 176 -----KNPDGHMDGTLTNGVLVHMPREG-----FTEE 202
A;Molecule type: mRNA		DB 73 ALNPLRKQKRCGH-PGDPGFTFL-TGNNVFEVGVAVTCMFGQQLGTRINVR 129
A;Residues: 27-76 <SC2>		OY 203 SORGVWRBISVCGDVYTRERTSAQORGKLVESETN-----VHQDGLSLIDLC 249
A;Cross-references: UNIPARC:UPI0001742EA		DB 130 DTGWTNDIPICEVKCLPV---APENGKIVSSAMEPDRTEHFGQAVRFVCNSGYKE-- 185
A;Note: this is a partial sequence of an alternatively spliced 1.8 kilobase mRNA that is		QY 250 GATLIMTADGLFHTPTQKHLRQBNINAAPQCPVGLNTAFPSNRKVKEVQPA 309
R;Sim, R.B.; Discipio, R.G.		DB 186 GDEMHCSDDGWSKEKPCV---BISCKSPDVING-----SPISQKLYKNERFQ 234
OY 310 YLSCGHVFGYHMGHRSDETEANERECPCMCRVY---GPYVP-----LWLG 350		DI 235 Y-KCNGVGEYSERGDAVCTESGRPILPSCEBKSCDNPYTPNGDYSPLRKHRTGDETYQ 293

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Page 7

Qy	351	CEAGFVYDAGPPHTAFTPCCHV---CSEKSAKY	380
Db	294	CRNGFYPATRGNTAKCTSTWIPAPRCTLXPCDY	327

Search completed: March 1, 2006, 21:00:48  
Job time : 42 secs

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GenCore version 5.1.7  
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## OM protein - protein search, using sw model

Run on: March 1, 2006, 20:52:46 ; Search time 185 Seconds

(without alignments)  
99.509 Million cell updates/sec

Title: US-10-041-030-4

perfect score: 2290

Sequence: 1 MFSPGQEBEHCAPNKPKVKG. .... ATOLVGEONCNIKLIPOGPID 420

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Maximum Match 100%  
Listing first 45 summaries

A\_Geneseq\_21:\*

1: geneseqD19808:\*

2: geneseqD19988:\*

3: geneseqD20008:\*

4: geneseqD20018:\*

5: geneseqD20028:\*

6: geneseqD20038:\*

7: geneseqD20038b:\*

8: geneseqD20058:\*

9: geneseqD20058b:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result NO. Score Query Match Length DB ID Description

1 2290 100.0 420 5 ABB78077

2 2290 100.0 420 5 ABB17522

3 2290 100.0 420 6 ABR1083

4 2290 100.0 420 7 ADC31180

5 2283 99.7 420 5 ABB07922

6 2283 99.7 420 8 ADP8671

7 2175.5 95.0 419 5 ABB07921

8 2175.5 95.0 419 6 ADP8669

9 2111.5 92.2 419 6 ABR1082

10 1917 83.7 418 5 ABB07920

11 1917 83.7 418 5 ADP17518

12 1917 83.7 418 6 ABU00017

13 1917 83.7 418 8 ADP53103

14 1917 83.7 418 8 ADP4405

15 1917 83.7 418 8 ADP48667

16 1917 83.7 418 8 ADP56420

17 1917 83.7 418 9 ADP24929

18 1917 83.7 418 9 ADY20614

19 1917 83.7 418 9 ADY17390

20 1916 83.7 418 5 ADQ17515

21 1913 83.5 418 5 ABB078078

22 1912 83.5 418 5 ABB07919

23 1912 83.5 418 8 ADP48555

24 1910 83.4 418 5 AAO17519

Post: 1582.5

Score: 69.1

Time: 415

CPU: 8

Memory: ADD44009

Disk: 5

Network: AAO17516

Serial: 5

Parallel: AAO17517

Job: 1482.5

Status: 64.7

Priority: 406

Version: 7

Build: ADB65774

Module: ABB94502

Library: AAG67255

Protocol: ABB61353

Protocol: ABB07924

Protocol: 39

Protocol: 40

Protocol: 41

Protocol: 42

Protocol: 43

Protocol: 44

Protocol: 45

Protocol: 1077

Protocol: 47.0

Protocol: 241

Protocol: 4

Protocol: ABC04494

Post: 1392

Score: 56.9

Time: 424

CPU: 4

Memory: ABB61353

Disk: 5

Network: ADP48676

Serial: 56.9

Parallel: 320

Job: 4

Status: 56.8

Priority: 320

Version: AAM93893

Build: ADI31994

Protocol: ABB07925

Protocol: ADP48677

Protocol: 455

Protocol: 46

Protocol: ADG32882

Protocol: 1102

Protocol: 48.1

Protocol: 196

Protocol: 49

Protocol: 1077

Protocol: 47.0

Protocol: 241

Protocol: 4

Protocol: ABC04494

Post: 1302

Score: 56.9

Time: 424

CPU: 5

Memory: ABB61353

Disk: 5

Network: ADP48676

Serial: 56.9

Parallel: 320

Job: 4

Status: 56.8

Priority: 320

Version: AAM93893

Build: ADI31994

Protocol: ABB07925

Protocol: ADP48677

Protocol: 455

Protocol: 46

Protocol: ADG32882

Protocol: 1102

Protocol: 48.1

Protocol: 196

Protocol: 49

Protocol: 1077

Protocol: 47.0

Protocol: 241

Protocol: ABC04494

Post: 1302

Score: 56.9

Time: 424

CPU: 5

Memory: ABB61353

Disk: 5

Network: ADP48676

Serial: 56.9

Parallel: 320

Job: 4

Status: 56.8

Priority: 320

Version: AAM93893

Build: ADI31994

Protocol: ABB07925

Protocol: ADP48677

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CPU: 5

Memory: ABB61353

Disk: 5

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Protocol: ADP48677

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Protocol: ABC04494

Post: 1302

Score: 56.9

Time: 424

CPU: 5

Memory: ABB61353

Disk: 5

Network: ADP48676

Serial: 56.9

Parallel: 320

Job: 4

Status: 56.8

Priority: 320

Version: AAM93893

Build: ADI31994

Protocol: ABB07925

Protocol: ADP48677

Protocol: 455

Protocol: 46

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Protocol: 1102

Protocol: 48.1

Protocol: 196

Protocol: 49

Protocol: 1077

Protocol: 47.0

Protocol: 241

Protocol: ABC04494

Post: 1302

Score: 56.9

Time: 424

CPU: 5

Memory: ABB61353

Disk: 5

Network: ADP48676

Serial: 56.9

Parallel: 320

Job: 4

Status: 56.8

Priority: 320

Version: AAM93893

Build: ADI31994

Protocol: ABB07925

Protocol: ADP48677

Protocol: 455

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Protocol: ADG32882

Protocol: 1102

Protocol: 48.1

Protocol: 196

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Protocol: 1077

Protocol: 47.0

Protocol: 241

Protocol: ABC04494

Post: 1302

Score: 56.9

Time: 424

CPU: 5

Memory: ABB61353

Disk: 5

Network: ADP48676

Serial: 56.9

Parallel: 320

Job: 4

Status: 56.8

Priority: 320

Version: AAM93893

Build: ADI31994

Protocol: ABB07925

Protocol: ADP48677

Protocol: 455

Protocol: 46

Protocol: ADG32882

Protocol: 1102

Protocol: 48.1

Protocol: 196

Protocol: 49

Protocol: 1077

Protocol: 47.0

Protocol: 241

Protocol: ABC04494

Post: 1302

Score: 56.9

Time: 424

CPU: 5

Memory: ABB61353

Disk: 5&lt;/

CC	t tract	PT	Diagnosis of neurodegenerative disease, comprises detecting level of M30-family proteins.
XX	SQ	XX	Claim 2; Page 116-117; 130pp; German.,
Query Match	100.0% ; Score 2290; DB 5; Length 420;	CC	The present invention relates to a method of diagnosing neurodegenerative diseases, comprising determining the concentration of a protein in a body sample, where the protein may be M30 or a variant thereof, M31, M32 or M33. The method is used to diagnose neurodegenerative diseases, particularly stroke but also e.g. fragile X syndrome, Huntington's, parkinson's and Alzheimer's diseases, multiple sclerosis etc. Also, overexpression of M31 can be used for diagnosis of carcinoma and sarcoma, especially ovarian cancer. The proteins can be used to identify specific ligands, potentially useful for treating neurodegeneration, immune-system disorders (e.g. autoimmune diseases, allergy, viral infection, leukaemia, inflammation etc.), carcinoma and sarcoma. Inhibitors of the interaction between the proteins and the protein kinase IRAK-1 can be used to treat neurodegeneration. The present sequence is a protein used in the method of the invention
Best Local Similarity	100.0% ; Pred. No. 2. 8e-226; Indels 0; Gaps 0;	CC	CC
Matches	420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	CC
OY	1 MFSPGQEBEHCAPEVKVIGELVLVYNGALPNQDRGRKSFRALYKRPKANGVKPSTVH 60	CC	CC
Db	1 MFSPGQEBEHCAPEVKVIGELVLVYNGALPNQDRGRKSFRALYKRPKANGVKPSTVH 60	CC	CC
OY	61 VISTPOASKAISCKGQHSISYTLSRNQTIVVEYTHDKDMDQVRGSTESPIDFVMTI 120	CC	CC
Db	61 VISTPOASKAISCKGQHSISYTLSRNQTIVVEYTHDKDMDQVRGSTESPIDFVMTI 120	CC	CC
OY	121 SGSONTDEAQITQSTISRPA�CIVCDRNEPYTARIFAGFDSKSNIFLGEKAJKWKGPDG 180	CC	CC
Db	121 SGSONTDEAQITQSTISRPA�CIVCDRNEPYTARIFAGFDSKSNIFLGEKAJKWKGPDG 180	CC	CC
OY	181 HMDGLTTNGVLYMPRGFTESOPGVWREISVGDVYTIRTRSAQORGKLVESTNVL 240	CC	CC
Db	181 HMDGLTTNGVLYMPRGFTESOPGVWREISVGDVYTIRTRSAQORGKLVESTNVL 240	CC	CC
OY	241 QDSLIDICGATLWRADGLFPTOKHIEALROEINAAQPCPGVNLTAFFPSINKE 300	CC	CC
Db	241 QDSLIDICGATLWRADGLFPTOKHIEALROEINAAQPCPGVNLTAFFPSINKE 300	CC	CC
OY	301 VWEERKQPAWYLSCSCKHVGHMGHSRDTTEAMERECPCMRTVGPVYLWLGCAGFYVDAG 360	CC	CC
Db	301 VWEERKQPAWYLSCSCKHVGHMGHSRDTTEAMERECPCMRTVGPVYLWLGCAGFYVDAG 360	CC	CC
OY	361 PPTHAFTPCFGHVSESEKSAKTYWSQIPLPHGTHAFHAACPFCAATOLVGEONCILKUFIQPID 420	CC	CC
Db	361 PPTHAFTPCFGHVSESEKSAKTYWSQIPLPHGTHAFHAACPFCAATOLVGEONCILKUFIQPID 420	CC	CC
<hr/>			
RESULT 2		Do	Query Match 100.0% ; Score 2290; DB 5; Length 420;
RAO17522	ID AAO17522 standard; protein; 420 AA.	OY	Best Local Similarity 100.0% ; Pred. No. 2. 8e-226; Indels 0; Gaps 0;
XX	AC AAO17522;	Db	Matches 420; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	DT 19-JUL-2002 (first entry)	OY	1 MFSPGQEBEHCAPEVKVIGELVLVYNGALPNQDRGRKSFRALYKRPKANGVKPSTVH 60
DB	Human M33 protein SEQ ID NO: 16.	Db	1 MFSPGQEBEHCAPEVKVIGELVLVYNGALPNQDRGRKSFRALYKRPKANGVKPSTVH 60
XX		OY	61 VISTPOASKAISCKGQHSISYTLSRNQTIVVEYTHDKDMDQVRGSTESPIDFVMTI 120
XX		Db	61 VISTPOASKAISCKGQHSISYTLSRNQTIVVEYTHDKDMDQVRGSTESPIDFVMTI 120
XX		OY	121 SGSONTDEAQITQSTISRPA�CIVCDRNEPYTARIFAGFDSKSNIFLGEKAJKWKGPDG 180
XX		Do	121 SGSONTDEAQITQSTISRPA�CIVCDRNEPYTARIFAGFDSKSNIFLGEKAJKWKGPDG 180
XX		OY	181 HMDGLTTNGVLYMPRGFTESOPGVWREISVGDVYTIRTRSAQORGKLVESTNVL 240
XX		Db	181 HMDGLTTNGVLYMPRGFTESOPGVWREISVGDVYTIRTRSAQORGKLVESTNVL 240
XX		OY	241 QDSLIDICGATLWRADGLFPTOKHIEALROEINAAQPCPGVNLTAFFPSINKE 300
XX		Db	241 QDSLIDICGATLWRADGLFPTOKHIEALROEINAAQPCPGVNLTAFFPSINKE 300
XX		OY	301 VWEERKQPAWYLSCSCKHVGHMGHSRDTTEAMERECPCMRTVGPVYLWLGCAGFYVDAG 360
XX		Db	301 VWEERKQPAWYLSCSCKHVGHMGHSRDTTEAMERECPCMRTVGPVYLWLGCAGFYVDAG 360
XX		OY	361 PPTHAFTPCFGHVSESEKSAKTYWSQIPLPHGTHAFHAACPFCAATOLVGEONCILKUFIQPID 420
XX		Db	361 PPTHAFTPCFGHVSESEKSAKTYWSQIPLPHGTHAFHAACPFCAATOLVGEONCILKUFIQPID 420
<hr/>			
RESULT 3		OS Homo sapiens.	OS Homo sapiens.
ARR41083	ID ABR41083 standard; protein; 420 AA.	XX	OS Homo sapiens.
XX	XX	XX	XX
XX	XX	XX	XX
PP 07-SEP-2001; 2001WO-EP010366.	DT 22-MAY-2003 (first entry)	XX	XX
XX	XX	XX	XX
PR 07-SEP-2000; 2000US-00657479.	DB Human MAP kinase cascade activator #59.	XX	XX
XX		XX	
PA (AXAR-) AXARON BIOSCIENCE AG.	KW Human; Elk1 phosphorylation; Elk1 phosphorylation kinase; virucide; antiinflammatory; immunomodulator; cytotoxic; antiallergic; anti-HIV; antiarthritic; antidiabetic; antiasthmatic; gene therapy; inflammation; autoimmune disease; viral disease; cancer; diabetes; rheumatoid arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis; IGA nephritis.	XX	XX
XX		XX	
XX		XX	
PT Schneider A, Hienisch H, Rosner M, Klugmann M, Naim J; PI Eisenhardt G, Kuner R, Lanahan A, Worley P, Spielvogel D, Scheek S; XX DR WI; 2002-29287/33.	XX	XX	XX
DR N-PSDB; AAL-6323.	XX	XX	XX

XX  
XX  
PN WO2003008589-A1.  
XX  
PD 30-JAN-2003.  
XX  
PR 15-JUL-2002; 2002WO-JP007174.  
XX  
PR 18-JUL-2001; 2001JP-00218204.  
PR 21-JAN-2002; 2002JP-00012176.  
PA (ASAHI ) ASAI KASEI KOCYO KK.  
XX  
PT Matsuzaki, O., Matuda A., Nagano Y., Suzuki N.;  
XX  
WPI; 2003-229582/22.  
DR N-PSDB; ADC2349.  
XX  
PT Elk1 phosphorylation-associated gene and its encoded protein with MAP kinase cascade effect, applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer.  
XX  
PS Claim 1; Page 640-643; 762pp; Japanese.  
XX  
CC The invention relates to a novel purified protein having Elk1 phosphorylation activity and/or an activity of activating Elk1 phosphorylation kinase. A protein of the invention has antiinflammatory, immunomodulator, virucide, cytostatic, antiallergic, antirheumatic, antiarthritic, antidiabetic, antiasthmatic, and anti-HIV activity. The polynucleotides may have a use in gene therapy. The gene and its encoded protein are applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer such as rheumoid arthritis, diabetes, asthma, allergic rhinitis, AIDS, viral hepatitis and IGA nephritis. The present sequence is used in the exemplification of the invention.  
XX  
SQ Sequence 420 AA:  
Query Match 100.0%; Score 2290; DB 6; Length 420;  
Best Local Similarity 100.0%; Pred. No. 2.8e-226; Mismatches 0; Indels 0; Gaps 0;  
Matches 420; Conservative 0; Pairs 0; Gaps 0;  
OY 1 MFSPGQEEMCAPNPKEPVKVKGELVVLGVNGALPNQDRGRKSRLA  
Db 1 MPSFGQEEBRCAPNPKEPVKVKGELVVLGVNGALPNQDRGRKSRLA  
OY 61 VISPTQASKRAISCKGHSISYTSRNTQTVWEYTHDKDIDMFOGRSSESPIPVYVTTI 120  
Db 61 VISPTQASKRAISCKGHSISYTSRNTQTVWEYTHDKDIDMFOGRSSESPIPVYVTTI 120  
OY 121 SGSGNTDRAQTQFOTISFACTIVCDRNEPYTARIFAGPDSKSNIPGEAKWKWDG 180  
Db 121 SGSGNTDRAQTQFOTISFACTIVCDRNEPYTARIFAGPDSKSNIPGEAKWKWDG 180  
OY 181 HMDGLTTNGVLMMPRGFTTESOPGVWRREISVGDVYTLETRSAORGKLVESETAVL 240  
Db 181 HMDGLTTNGVLMMPRGFTTESOPGVWRREISVGDVYTLETRSAORGKLVESETAVL 240  
OY 241 QDSESLIDGAGATLWRTADGLPHPTOKHIEARQEINARPOCPVGNLTAPSINKE 300  
Db 241 QDSESLIDGAGATLWRTADGLPHPTOKHIEARQEINARPOCPVGNLTAPSINKE 300  
OY 301 VWEKQPMVYLSCSGHVGHTMGHRSDAERKPCPMTGTVGPPVPLMGEAGFYDAG 360  
Db 301 VWEKQPMVYLSCSGHVGHTMGHRSDAERKPCPMTGTVGPPVPLMGEAGFYDAG 360  
OY 361 PPTHAFTPCGHVCSEKSAKWWQSQPLPHGTHAFAACPCATQVGEONCIIKUHQGD 420  
Db 361 PPTHAFTPCGHVCSEKSAKWWQSQPLPHGTHAFAACPCATQVGEONCIIKUHQGD 420  
RESULT 4  
ADC31180

ID ADC31180 standard; protein; 420 AA.  
XX  
XX  
XX ADC31180;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human novel polypeptide sequence, SEQ ID NO:1262.  
XX  
KW Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; anti-parkinsonian; nootropic; neuroprotective; anti-naeamic; anticoagulant; thrombolytic; pulmonary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic; gene therapy; chromosome 14q21.  
XX  
OS Homo sapiens.  
XX  
PN WO2003029271-A2.  
XX  
PR 24-SEP-2001; 2001US-0324631P.  
PD 10-APR-2003.  
XX  
PR 24-SEP-2002; 2002WO-US030474.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
Tang TW, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T, Zhou P, Ghosh M, Wang D, Ma Y, Abundi V, Wang Z, Weng G; Haley-Vicente D, Drmanac RT;  
XX  
WPI; 2003-371981/35.  
DR N-PSDB; ADC30209.  
XX  
PT New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer.  
XX  
PS Claim 20; SEQ ID NO 1262; 1185pp; English.  
XX  
CC The invention relates to 971 novel human cDNA sequences (ADC29919-ADC3089) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention, the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of preventing, treating or ameliorating a medical condition, kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention (ADC31861-ADC32677) and the polypeptides encoded by the contigs (ADC3268-ADC3394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's disease and other neurodegenerative diseases, anemia, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or cancer. The nucleic acids may also be used as hybridisation probes or primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, and as food supplements. The present sequence represents a specifically claimed human polypeptide sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but

CC was obtained in electronic format directly from WIPO at  
 CC [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
 XX  
 SQ Sequence 420 AA:

PT transcription.  
 XX  
 Claim 1; Page 61-63; 70pp; English.

Query Match 100.0%; Score 2290; DB 7; Length 420;  
 Best Local Similarity 100.0%; Pred. No. 2, 8e-226; Mismatches 0; Indels 0; Gaps 0;  
 Matches 420; Conservative 0; Nucleotides 0; Polypeptides 0;  
 QY 1 MSPGQEEHCAKEPKVYGEVLVGLNGALPNGDRGRKSRPALKYRKPKANGVKESTVH 60  
 DB 1 MSPGQEEHCAKEPKVYGEVLVGLNGALPNGDRGRKSRPALKYRKPKANGVKESTVH 60  
 QY 61 VISTPQASKAISCKGKHSISYTSLRNQTVVYTHDKDTDMQVRGSTESPIDFVVTI 120  
 DB 61 VISTPQASKAISCKGKHSISYTSLRNQTVVYTHDKDTDMQVRGSTESPIDFVVTI 120  
 QY 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYPTARIFAAFGFDSKSKNITLGKAKWKPDG 180  
 DB 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYPTARIFAAFGFDSKSKNITLGKAKWKPDG 180  
 QY 181 HMDGLTNGVLMHPKGFTESQPGWREISVCGDVTLRETSAQORGKLVESTNVL 240  
 DB 181 HMDGLTNGVLMHPKGFTESQPGWREISVCGDVTLRETSAQORGKLVESTNVL 240  
 QY 241 QDSSLIDICGATILWRADGLFHTPTQHKIAEINARRQCPVGNTLAFFSINKE 300  
 DB 241 QDSSLIDICGATILWRADGLFHTPTQHKIAEINARRQCPVGNTLAFFSINKE 300  
 QY 301 VVERKQPWAVLSCGHVHGHNWGRSDTEANERECPMORTVGPYVPLWLGCAGFYVDAG 360  
 DB 301 VVERKQPWAVLSCGHVHGHNWGRSDTEANERECPMORTVGPYVPLWLGCAGFYVDAG 360  
 QY 361 PPTHAFTPCGHVSEKSAKYSQIPLPHTAFAACPCATOLVGEONCILKLIQGPID 420  
 DB 361 PPTHAFTPCGHVSEKSAKYSQIPLPHTAFAACPCATOLVGEONCILKLIQGPID 420  
 RESULT 5

ID ABB07922 standard; protein; 420 AA.  
 AC ABB07922;  
 XX DT 30-JUL-2002 (first entry)  
 XX DE Human Pellino-2 polypeptide.  
 XX KW Nuclear factor-kappaB; NF- kappaB; p38; pellino; interleukin-1; virucide; antibacterial; fungicide; protozoacide; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antiatherosclerotic; neuroprotective; mototropic; antiulcer; human; pellino-2.  
 XX OS Homo sapiens.  
 XX PN WO200183739-A2.  
 XX PD 08-NOV-2001.  
 XX PR 27-APR-2001; 2001WO-US013676.  
 XX PR 28-APR-2000; 2000US-0200198P.  
 XX PA (IMMV ) IMMUNEX CORP.  
 XX PT Bird TA, Cosman DJ;  
 XX DR WPI; 2002-066532/09.  
 XX DR N-FSDB; ABL58449.  
 XX PT New Pellino polypeptides for identifying compounds that alter polypeptide activity, treating pathogenic infection or inhibiting apoptosis, are capable of stimulating nuclear factor-kappaB- or p38-dependent

PT transcription.  
 XX  
 Claim 1; Page 61-63; 70pp; English.  
 The invention provides polypeptides capable of stimulating nuclear factor (NF)-kappaB-dependent transcription or p38-dependent transcription inhibitors that alter the pellino polypeptide and pellino identifying modulators that alter the pellino polypeptide and pellino compounds that inhibit the binding activity of the polypeptides and to study cell-signal transduction. They are useful for preventing or treating infection by a pathogen such as virus, bacterial, fungi, algae or protozoa, or inhibiting apoptosis. Dominant-negative pellino polypeptides are useful for treating inflammatory conditions such as asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis and Alzheimer's disease, and also for inhibiting mitogen activated protein (MAP) kinase-activated pathways. Pellino polypeptides and polynucleotides are useful to identify small molecule inhibitors of protein association or function of Pellino, and other molecules involved in interleukin (IL)-1 signaling. The present sequence represents a human pellino-2 polypeptide

SQ Sequence 420 AA;

Query Match 99.7%; Score 2283; DB 5; Length 420;  
 Best Local Similarity 99.8%; Pred. No. 1, 5e-225; Mismatches 1; Indels 0; Gaps 0;  
 Matches 419; Conservative 0; Nucleotides 0; Polypeptides 0;  
 QY 1 MSPGQEEHCAKEPKVYGEVLVGLNGALPNGDRGRKSRPALKYRKPKANGVKESTVH 60  
 DB 1 MSPGQEEHCAKEPKVYGEVLVGLNGALPNGDRGRKSRPALKYRKPKANGVKESTVH 60  
 QY 61 VISTPQASKAISCKGKHSISYTSLRNQTVVYTHDKDTDMQVRGSTESPIDFVVTI 120  
 DB 61 VISTPQASKAISCKGKHSISYTSLRNQTVVYTHDKDTDMQVRGSTESPIDFVVTI 120  
 QY 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYPTARIFAAFGFDSKSKNITLGKAKWKPDG 180  
 DB 121 SGSQNTDEAQITOSTISRFACTIVCDRNPYPTARIFAAFGFDSKSKNITLGKAKWKPDG 180  
 QY 181 HMDGLTNGVLMHPKGFTESQPGWREISVCGDVTLRETSAQORGKLVESTNVL 240  
 DB 181 HMDGLTNGVLMHPKGFTESQPGWREISVCGDVTLRETSAQORGKLVESTNVL 240  
 QY 241 QDSSLIDICGATILWRADGLFHTPTQHKIAEINARRQCPVGNTLAFFSINKE 300  
 DB 241 QDSSLIDICGATILWRADGLFHTPTQHKIAEINARRQCPVGNTLAFFSINKE 300  
 QY 301 VVERKQPWAVLSCGHVHGHNWGRSDTEANERECPMORTVGPYVPLWLGCAGFYVDAG 360  
 DB 301 VVERKQPWAVLSCGHVHGHNWGRSDTEANERECPMORTVGPYVPLWLGCAGFYVDAG 360  
 QY 361 PPTHAFTPCGHVSEKSAKYSQIPLPHTAFAACPCATOLVGEONCILKLIQGPID 420  
 DB 361 PPTHAFTPCGHVSEKSAKYSQIPLPHTAFAACPCATOLVGEONCILKLIQGPID 420  
 RESULT 6

ID ADP48671 standard; protein; 420 AA.  
 AC ADP48671;  
 XX DT 09-SEP-2004 (first entry)  
 XX DE Human Pellino-2 protein SEQ ID NO:8.  
 XX DS3  
 XX KW nuclear factor kappa B dependent transcription inhibitor;  
 KW NF-kB-dependent transcription inhibitor;  
 KW p38-dependent transcription inhibitor; Pellino-1;  
 KW interleukin 1 receptor-associated kinase 4;  
 KW IL-1 receptor-associated kinase 4; IRAK-4; antiarteriosclerotic;  
 KW antiarthritic; antiasthmatic; antiinflammatory; antirheumatic; antiulcer;

KW gastrointestinal; neuroprotective; nootropic; IL-1 antagonist;  
 KW IIRK protein kinase family inhibitor;  
 KW NF kappa B inducing kinase inhibitor; asthma; rheumatoid arthritis;  
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW atherosclerosis; Alzheimer's disease; human; Pellino-2; chromosome 14.  
 OS Homo sapiens.  
 XX WO2004053092-A2.  
 XX 24-JUN-2004.  
 XX 09-DEC-2003; 2003WO-US039188.  
 XX 11-DEC-2002; 2002US-00317250.  
 PA (IMMUNEX CORP.)  
 PA (CLEV-.) CLEVELAND CLINIC FOUND.  
 XX  
 PT Bird TA, Cosman DJ, Li X;  
 XX DR WPI; 2004-480927/45.  
 XX DR N-PSDB; ADP48670.  
 XX  
 PT identifying inhibitors of IL-1 signaling, useful for treating e.g.,  
 PT asthma, and rheumatoid arthritis, comprises assaying the association of a  
 PT Pellino-1 polypeptide with IRAK4 in the presence of a test compound.  
 XX  
 PS Example 1; SEQ ID NO 8; 81pp; English.  
 XX  
 CC The present invention describes a method for identifying compounds (C)  
 CC that inhibit nuclear factor kappa B (NF- $\kappa$ B)-dependent transcription or  
 CC p38-dependent transcription. The method comprises: (1) mixing a test  
 CC compound with a Pellino-1 polypeptide; (2) assaying the association of  
 CC the Pellino-1 polypeptide with IL-1 receptor-associated kinase 4 (IRAK-4)  
 CC in the presence of the test compound; and (3) determining whether the  
 CC test compound inhibits the association of the Pellino-1 polypeptide with  
 CC a binding partner. Also described: (1) an inhibitory nucleic acid that  
 CC binds to a nucleic acid encoding an amino acid sequence as described  
 above, where the presence of the inhibitory nucleic acid within a cell  
 CC inhibits the association of Pellino-1 with IRAK-4; and (2) an inhibitory  
 CC polypeptide comprising an antibody fragment that binds to a polypeptide  
 CC comprising an amino acid sequence as described above, where the presence  
 CC of the inhibitory polypeptide within a cell inhibits the association of  
 CC Pellino-1 with IRAK-4. (C) have antirheumatoclerotic, antiarthritic,  
 CC antiasthmatic, antiinflammatory, antirheumatic, antiluler,  
 CC gastrointestinal, neuroprotective and nootropic activities, and can be  
 CC used as an IL-1 antagonist, IRAK protein kinase family inhibitor, and NF  
 CC kappa B inducing kinase inhibitor. The methods and compositions of the  
 CC present invention are useful for the prevention and/or treatment of  
 CC diseases or conditions associated with aberrant expression or activity of  
 CC the Pellino-1 polypeptide, such as asthma, rheumatoclerotic, antiarthritic,  
 CC atherosclerosis and Alzheimer's disease. Crohn's disease, ulcerative colitis,  
 CC human Pellino-2, which is used in the exemplification of the present  
 CC invention. The human Pellino-2 gene is located on chromosome 14, more  
 CC specifically to 14q24.3.  
 XX  
 SQ Sequence 420 AA:  
 Query Match 99.7%; Score 2283; DB 8; Length 420;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-225;  
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 MFSRQGEECAPNPGPVKGELVNGALPQDRGRKSRALYKPKKANVKPKSTWH 60  
 OY 1 MFSRQGEECAPNPGPVKGELVNGALPQDRGRKSRALYKPKKANVKPKSTWH 60  
 OY 61 VISTPOASKAIICKQHQSISYTSLSRNQTVWVTHDKOTDMRQGRSSTSPDPWMDT 120  
 OY 61 VISTPOASKAIICKQHQSISYTSLSRNQTVWVTHDKOTDMRQGRSSTSPDPWMDT 120  
 DB 121 SGSQNTDRAQQTOSTSRPACIVCDENPTYARIFAGFDSSKNIFLGEKAQKWNPDG 180  
 DB 181 HMDGLTNGVLVMPREGFTERSQPGWRETSVCGDVYTLBETRSAQQRGLVSETNVL 240  
 DO 181 HMDGLTNGVLVMPREGFTERSQPGWRETSVCGDVYTLBETRSAQQRGLVSETNVL 240  
 OY 241 QDSSLIDPGATILWRADGLHTPTOKHIALEQNEAARQCPQVGLNTAFLPSINKE 300  
 DO 241 QDSSLIDPGATILWRADGLHTPTOKHIALEQNEAARQCPQVGLNTAFLPSINKE 300  
 OY 301 VTERKQPAVLSQGHVIGXNHGRSITBANEBCRMRTGTYVPLHGEAGFYDAG 360  
 DO 301 VTERKQPAVLSQGHVIGXNHGRSITBANEBCRMRTGTYVPLHGEAGFYDAG 360  
 OY 361 PPTHAFTPCGHVSEKARYWQIPLPHGTHAFAACFCATOLVSGRNCKLIFQFID 420  
 DO 361 PPTHAFTPCGHVSEKARYWQIPLPHGTHAFAACFCATOLVSGRNCKLIFQFID 420  
 RESULT 7  
 ID ABB07921 standard; protein: 419 AA.  
 XX  
 AC ABB07921;  
 XX DT 30-JUL-2002 (first entry)  
 DB Murine pellino-2 polypeptide.  
 XX  
 KW Nuclear factor-kappaB; NF-kappaB; p38; pellino; interleukin-1; virucide;  
 KW antibacterial; fungicide; protozoacide; antiasthmatic; antirheumatic;  
 KW antiarthritic; antiinflammatory; antiatherosclerotic; neuroprotective;  
 KW nootropic; antiulcer; mouse; pellino-2.  
 XX OS Mus musculus.  
 XX PN WO2004053092-A2.  
 XX DT 08-NOV-2001.  
 XX  
 PF 27-APR-2001; 2001WO-US013676.  
 PR 28-APR-2000; 2000US-0200198B.  
 PA (IMMUNEX CORP.)  
 XX  
 PT Bird TA, Cosman DJ;  
 XX DR WPI; 2002-066532409.  
 XX DR N-PSDB; ABLS8448.  
 XX  
 PT New Pellino polypeptides for identifying compounds that alter polypeptide  
 PT activity, treating pathogenic infection or inhibiting apoptosis,-are  
 PT capable of stimulating nuclear factor-kappaB- or p38-dependent  
 PT transcription.  
 XX  
 PS Example; Page 59-60; 70pp; English.  
 XX  
 CC The invention provides polypeptides capable of stimulating nuclear factor  
 CC (NF)- $\kappa$ B-dependent transcription or p38-dependent transcription,  
 CC referred as Pellino polypeptides. The pellino polypeptides are useful for  
 CC identifying modulators that alter the pellino Polypeptide and pellino  
 CC dominant-negative activators. They are also useful for identifying  
 CC compounds that inhibit the binding activity of the polypeptides and to  
 CC study cell signal transduction. They are useful for preventing or  
 CC treating infection by a pathogen such as virus, bacterial, fungi, algae  
 CC or protozoa, or inhibiting apoptosis. Dominant-negative pellino  
 CC polypeptides are useful for treating inflammatory conditions such as  
 CC asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's  
 CC disease, ulcerative colitis, atherosclerosis and Alzheimer's disease, and  
 CC also for inhibiting mitogen activated protein (MAP) kinase-activated  
 pathways. Pellino polypeptides and polynucleotides are useful to identify

CC small molecule inhibitors of protein association or function of Pellino,  
 CC and other molecules involved in interleukin (IL)-1 signaling. The present  
 CC sequence represents a murine Pellino-2 polypeptide

XX sequence 419 AA;

Query Match 95.0%; Score 2175.5; DB 5; Length 419;  
 Best Local Similarity 95.0%; Pred. No. 1.; e-214; Mismatches 10; Indels 1; Gaps 1;  
 Matches 399; Conservative 95.0%; Pred. No. 1.; e-214; Mismatches 10; Indels 1; Gaps 1;  
 XX

QY 1 MFSPGQEENCAPNCEPKVKIGELVLYNGALPNDGRGRKSFALEYKRPKANGYKPSTH 60  
 Db 1 MFSPGQEERSAPNCEPKVKIGELVLYNGALPNDGRGRKSFALEYKRPKANGYKPSTH 60  
 QY 61 VISPTQASKAISCKGHSISYTTSRNSQTVEYTHDKOTDMFOGRSSTSPIDRVPTI 120  
 Db 61 MVSPTQASKAISSSRGHHSISYTTSRNSQTVEYTHDKOTDMFOGRSSTSPIDRVPTI 120  
 QY 121 SGSONTDEAQITOSTISFACRIVCDRNEPYTARIFAGFDSSKNIFGEKAKWKNPDG 180  
 Db 121 SGSONTDEAQITOSTISFACRIVCDRNEPYTARIFAGFDSSKNIFGEKAKWKNPDG 180  
 QY 121 HMDGTTNGSVLVMERPGGTEESOPGVWREISVCGDVYTLRETRSAQORGKLVESETNVL 240  
 Db 121 HMDGTTNGSVLVMERPGGTEESOPGVWREISVCGDVYTLRETRSAQORGKLVESETNVL 240  
 QY 181 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 420  
 Db 181 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 420  
 QY 361 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 420  
 Db 361 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 420  
 QY 360 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 419  
 Db 360 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 419

RESULT 8

ADP48669

ID ADP48669 standard; protein; 419 AA.

XX

AC ADP48669;

XX

DT 09-SEP-2004 (first entry)

XX

DE Mouse Pellino-2 protein SEQ ID NO:6.

XX

KW nuclear factor kappa B dependent transcription inhibitor;

KW NF-kB-dependent transcription inhibitor; Pellino-1;

KW p38-dependent transcription inhibitor; Pellino-1;

KW interleukin 1 receptor-associated kinase 4;

KW IL-1 receptor-associated kinase 4;

KW antiarthritic; antiasthmatic; antiinflammatory;

KW antiarthritic; antiasthmatic; antiinflammatory; antirheumatic; antiulcer;

KW gastrointestinal; neuroprotective; nontropic; IL-1 antagonist;

KW IRAK protein kinase family inhibitor;

KW NF kappa B inducing kinase inhibitor; asthma; rheumatoid arthritis;

KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW atherosclerosis; Alzheimer's disease; mouse; Pellino-2.

XX

OS Mus musculus.

XX

PN WO2004053092-A2.

XX

PD 24-JUN-2004.

XX

PF 09-DEC-2003; 2003WO-US031918B.

XX

PR 11-DEC-2002; 2002US-00317250.

XX

(IMMUN ) IMMUNE CORP.

PA (CLEVELAND CLINIC FOUND.

XX

PI Bird TA, Cobman DJ, Li X;

XX

DR N-PSDB; ADP48668.

XX

PT Identifying inhibitors of IL-1 signaling, useful for treating e.g.,  
 PT asthma, and rheumatoid arthritis, comprises assaying the association of a  
 PT Pellino-1 polypeptide with TRAK-4 in the presence of a test compound.

XX

PS Example 1; SEQ ID NO 6; 81PP; English.

CC The present invention describes a method for identifying compounds (C)  
 CC that inhibit nuclear factor kappa B (NF- $\kappa$ B)-dependent transcription or  
 CC p38-dependent transcription. The method comprises: (1) mixing a test  
 CC compound with Pellino-1 polypeptide; (b) assaying the association of  
 CC the Pellino-1 polypeptide with IL-1 receptor-associated kinase 4 (TRAK-4)  
 CC in the presence of the test compound; and (c) determining whether the  
 CC test compound inhibits the association of the Pellino-1 polypeptide with  
 CC a binding partner. Also described: (1) an inhibitory nucleic acid that  
 CC binds to a nucleic acid encoding an amino acid sequence as described  
 CC above, where the presence of the inhibitory nucleic acid within a cell  
 CC inhibits the association of Pellino-1 with TRAK-4; and (2) an inhibitory  
 CC polypeptide comprising an antibody fragment that binds to a polypeptide  
 CC comprising an amino acid sequence as described above, where the presence  
 CC of the inhibitory polypeptide within a cell inhibits the association of  
 CC Pellino-1 with TRAK-4. (C) have antiarteriosclerotic, antiarthritic,  
 CC antiasthmatic, antiinflammatory, antirheumatic, antiulcer,  
 CC gastrointestinal, neuroprotective and nontropic activities, and can be  
 CC used as an IL-1 antagonist. TRAK protein kinase family inhibitor, and NF  
 CC kappa B inducing kinase inhibitor. The methods and compositions of the  
 CC present invention are useful for the prevention and/or treatment of  
 CC diseases or conditions associated with aberrant expression or activity of  
 CC the Pellino-1 polypeptide, such as asthma, rheumatoid arthritis,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC atherosclerosis and Alzheimer's disease. The present sequence represents  
 CC mouse Pellino-2, which is used in the exemplification of the present  
 CC invention.

XX

Sequence 419 AA;

Query Match 95.0%; Score 2175.5; DB 8; Length 419;  
 Best Local Similarity 95.0%; Pred. No. 1.; e-214; Mismatches 10; Indels 1; Gaps 1;  
 Matches 399; Conservative 95.0%; Pred. No. 1.; e-214; Mismatches 10; Indels 1; Gaps 1;  
 XX

QY 1 MFSPGQEENCAPNCEPKVKIGELVLYNGALPNDGRGRKSFALEYKRPKANGYKPSTH 60  
 Db 1 MFSPGQEERSAPNCEPKVKIGELVLYNGALPNDGRGRKSFALEYKRPKANGYKPSTH 60  
 QY 61 VISPTQASKAISCKGHSISYTTSRNSQTVEYTHDKOTDMFOGRSSTSPIDRVPTI 120  
 Db 61 MVSPTQASKAISSSRGHHSISYTTSRNSQTVEYTHDKOTDMFOGRSSTSPIDRVPTI 120  
 QY 121 SGSONTDEAQITOSTISFACRIVCDRNEPYTARIFAGFDSSKNIFGEKAKWKNPDG 180  
 Db 121 SGSONTDEAQITOSTISFACRIVCDRNEPYTARIFAGFDSSKNIFGEKAKWKNPDG 180  
 QY 181 HMDGTTNGSVLVMERPGGTEESOPGVWREISVCGDVYTLRETRSAQORGKLVESETNVL 240  
 Db 181 HMDGTTNGSVLVMERPGGTEESOPGVWREISVCGDVYTLRETRSAQORGKLVESETNVL 240  
 QY 180 HMDGTTNGSVLVMERPGGTEESOPGVWREISVCGDVYTLRETRSAQORGKLVESETNVL 239  
 Db 180 HMDGTTNGSVLVMERPGGTEESOPGVWREISVCGDVYTLRETRSAQORGKLVESETNVL 239  
 QY 241 QDSGLIDGATTLWRTAGLETPKTKTEALRQINARPQCPVGNTLAPSINRKE 300  
 Db 240 QDSGLIDGATTLWRTAGLETPKTKTEALRQINARPQCPVGNTLAPSINRKE 300  
 QY 301 WEEKQPMAYLSQCHVHGTHNGRSDEANERCPMCITVGPVPLMGCAEGFYVDAG 360  
 Db 301 WEEKQPMAYLSQCHVHGTHNGRSDEANERCPMCITVGPVPLMGCAEGFYVDAG 360  
 QY 361 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 420  
 Db 361 PPTHAFTPCGHVCSEKSAKWSQIPLPKGTHAFHACPCATOLVGEONCIRKLIQFGPID 419

RESULT 9  
 ABR41082 ID ABR41082 standard; protein; 419 AA.  
 XX AC ABR41082;  
 XX DT 22-MAY-2003 (first entry)  
 XX DE Mouse MAP kinase cascade activator #9.  
 XX KW Mouse; Elk1 phosphorylation; Elk1 phosphorylation kinase; virucide; antiinflammatory; immunomodulator; cytostatic; antiallergic; anti-HIV; antiarthritic; antidiabetic; antiasthmatic; gene therapy; inflammation; autoimmune disease; viral disease; cancer; diabetes; rheumatoïd arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis; IGA nephritis.  
 XX OS Mus musculus.  
 XX PN WO2003008589-A1.  
 XX PD 30-JAN-2003.  
 XX PP 15-JUL-2002; 2002WO-JP007174.  
 XX PR 18-JUL-2001; 2001JP-00218204.  
 XX PR 31-AUG-2001; 2001JP-00263450.  
 XX PR 21-JAN-2002; 2002JP-00012176.  
 XX PA (ASAH ) ASAHI KASRI KOGYO KK.  
 XX PT Matsuzaki O., Matsuda A., Nagano Y., Suzuki N.; DR WPI; 2003-2239582/22.  
 XX DR N-PSDB; ACC2348.  
 XX PS Claim 1; Page 628-630; 762pp; Japanese.  
 CC PT Elk1 phosphorylation-associated gene and its encoded protein having Elk1 phosphorylation activity and/or an activity of activating Elk1 phosphorylation kinase. A protein of the invention has antiinflammatory, immunomodulator, virucide, cytotoxic, antiallergic, antirheumatic, antiarthritic, antidiabetic, antiasthmatic, and anti-HIV activity. The polynucleotides may have a use in gene therapy. The gene and its encoded protein are applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer such as rheumatoïd arthritis, diabetes, asthma, allergic rhinitis, AIDS, viral hepatitis and IGA nephritis. The present sequence is used in the exemplification of the invention.  
 XX SQ Sequence 419 AA:

The invention relates to a novel purified protein having Elk1 phosphorylation activity and/or an activity of activating Elk1 phosphorylation kinase. A protein of the invention has antiinflammatory, immunomodulator, virucide, cytotoxic, antiallergic, antirheumatic, antiarthritic, antidiabetic, antiasthmatic, and anti-HIV activity. The polynucleotides may have a use in gene therapy. The gene and its encoded protein are applicable in diagnosis of and developing drugs for e.g. inflammations, autoimmune diseases, viral diseases and cancer such as rheumatoïd arthritis, diabetes, asthma, allergic rhinitis, AIDS, viral hepatitis and IGA nephritis. The present sequence is used in the exemplification of the invention.

Query Match Best Local Similarity 92.2%; Score 2111.5; DB 6; Length 419; Matches 388; Conservative 12; Mismatches 19; Indels 1; Gaps 1;

Ov 1 MFSPGQEEHCAPNKPKVKGELVYNGALPNQDRGRKSFRALKYKRPKANGKVKSTVH 60  
 Db 1 MFSPGQEEHCAPNKPKVKGELVYNGALPNQDRGRKSFRALKYKRPKANGKVKSTVH 60  
 Qv 61 VSPTRQASKAISCKGKHSISYTISLRSNQTVWYTHDKOTDMQYGRSSESPPFVMTI 120  
 61 MVSPTQASKAISCKGKHSISYTISLRSNQTVWYTHDKOTDMQYGRSSESPPFVMTI 120  
 Qv 121 SGSQNTDEAQITQSTISRACRVDRNPYTRIAFGPDSKKNIFGKAKWKPDG 180  
 121 SGSONDEAQITQSTISRACRVDRNPYTRIAFGPDSKKNIFGKAKWKPDG 179

RESULT 10  
 ABB07920 ID ABB07920 standard; protein; 418 AA.  
 XX AC ABB07920;  
 XX DT 30-JUL-2002 (first entry)  
 XX DB Human pellino-1 polypeptide.  
 XX PR Nuclear factor-kappaB; NF-kappaB; p38; pellino; interleukin-1; virucide; antibacterial; fungicide; protozoacide; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antiatherosclerotic; neuroprotective; nootropic; antiulcer; human; pellino-1.  
 XX OS Homo sapiens.  
 XX PN WO200113739-A2.  
 XX PD 08-NOV-2001.  
 XX PR 27-APR-2001; 2001WO-US013676.  
 XX PR 28-APR-2000; 2000US-0200138P.  
 XX PA (IMMUNEX CORP.  
 XX Bird TA, Cosman DJ;  
 XX DR WPI; 2002-066532/09.  
 XX DR N-PSDB; AB58447.  
 XX New Pelino polypeptides for identifying compounds that alter polypeptide activity, treating pathogenic infection or inhibiting apoptosis, are capable of stimulating nuclear factor-kappaB- or p38-dependent transcription.  
 XX PS Claim 1; Page 57-58; 70pp; English.

The invention provides polypeptides capable of stimulating nuclear factor (NF)-kappaB-dependent transcription or p38-dependent transcription, referred as Pelino polypeptides. The pelino polypeptides are useful for identifying modulators that alter the pelino polypeptide and pelino dominant-negative activity. They are also useful for identifying compounds that inhibit the binding activity of the polypeptides and to study cell-signal transduction. They are useful for preventing or treating infection by a pathogen such as virus, bacterial, fungi, algaee or protozoa, or inhibiting apoptosis. Dominant-negative pelino polypeptides are useful for treating inflammatory conditions such as asthma, rheumatoid arthritis, inflammatory bowel disease, Crohn's disease, ulcerative colitis, atherosclerosis and Alzheimer's disease, and also for inhibiting mitogen activated protein (MAP) kinase-activated pathways. Pelino polypeptides and polynucleotides are useful to identify small molecule inhibitors of protein association or function of Pelino, and other molecules involved in interleukin (IL)-1 signaling. The present sequence represents a human pellino-1 polypeptide



PN WO200274961-A1.  
 XX  
 PD 26-SEP-2002.  
 XX  
 PR 14-MAR-2002; 2002WO-US005109.  
 XX  
 PA (HYSE-) HYSQ INC.  
 Tang YT, Zhou P, Goodrich R, Asundi V, Zhang J, Zhao OA, Ren F;  
 PI Kue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
 WEhrman T, Wang J, Wang D, Drmanac RT;  
 WPI; 2003-040556/03.  
 DR N-FSDB; ABX05095.  
 XX  
 PT New isolated polypeptides and polymucleotides, useful for preventing,  
 PT treating or ameliorating medical conditions, such as cancer,  
 PT neurodegenerative disorders, lymphoid cell disorders, bone degenerative  
 PT disorders, and infections.  
 XX  
 PS Claim 9; SEQ ID NO 636; 235pp; English.  
 XX  
 CC The invention relates to human polymucleotides and the polypeptides they  
 encode. The polymucleotides and polypeptides are useful in diagnostics,  
 CC forensics, gene mapping, medical imaging, identification of mutations,  
 CC responsible for genetic disorders or other traits, assessing biodiversity  
 CC and producing many other types of data and products dependent on DNA and  
 CC amino acid sequences. They are also useful for preventing, treating or  
 CC ameliorating medical conditions, such as cancer, neurodegenerative  
 CC disorders (e.g., Parkinson's disease, Alzheimer's disease), lymphoid cell  
 CC disorders, osteoporosis, osteoarthritis, bone degenerative disorders,  
 CC periodontal disease, liver fibrosis, infections (e.g., viral, fungal or  
 CC bacterial) or autoimmune diseases (e.g., diabetes, atopic dermatitis).  
 CC Sequences ABG9888 and ABU0010-ABU0043 represent human  
 CC polypeptides of the invention. Note: The sequence data for this patent is  
 CC not represented in the printed specification but is based on sequence  
 CC information supplied by the European Patent Office  
 XX  
 Sequence 418 AA:  
 SQ Query Match 83.7%; Score 1917; DB 6; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 7.4e-188;  
 Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;  
 QY 1 MFSPGQEHCAPNKEPKVKGELVWGLNGALPENGDRGRKSRAKYKPKANGVKPVSTVH 60  
 Db 1 MFSPGQEHCAPNKEPKVKGELVWGLNGALPENGDRGRKSRAKYKPKANGVKPVSTVH 58  
 QY 61 VISTPOASKAISCKQHSISYTTSRNSQTVWVTHDKOTDMQVGRSTESPDPFWVTI 120  
 Db 59 IACTPOAKAISKDHSISYTTSRASQTVWVTHDSNIDMEQIGRSIESPDPFWVTI 118  
 QY 121 SGSONTDAQITOSTISFACRVCDRNPYTAIFAGFDSSKNIFGKAKWKPSDG 180  
 Db 119 PGQSNSDITQSVTISRACRICERNPPFTARIYANGFDSSSKNIFGKAKWKPSDG 178  
 QY 181 HMDGLITNGVLUVMPPRGSTEBSQGVWREISVGDDVTLERTRSDORGKVLESETVNL 240  
 Db 179 QMDGLITNGVLUVMPPRGSTEBSQGVWREISVGDDVTLERTRSDORGKVLESETVNL 238  
 QY 241 QDSLIDLGATLWRTADGLFPTQKHLRQEINARPOCPVGLNTLAPPSTINKE 300  
 Db 239 QDSLIDLGATLWRTADGLFPTQKHLRQEINARPOCPVGLNTLAPPSTINKE 298  
 QY 301 VVERKQPMWYLSSCCHVHGHNWGRSDTEANERCPMVRTGVPLMGCEAGFYVDAG 360  
 Db 239 VVERKQPMWYLSSCCHVHGHNWGRSDTEANERCPMVRTGVPLMGCEAGFYVDAG 358  
 QY 361 PPTHAFTPCGHVCSEBSKACYSWSOPLPHGTHAFHAACPCATOLVGBONCIKULFOQSDG 420  
 Db 359 PPTHAFTPCGHVCSEBSKACYSWSOPLPHGTHAFHAACPCAHOLAGEOGYIRLIFOQPLD 418  
 XX  
 RESULT 13  
 ADP83103  
 ID ADP83103 standard; protein: 418 AA.  
 XX  
 AC  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Human Pellino homologue 1, overexpressed in cancer.  
 XX KW Human; Pellino homologue 1; Pellinol; cancer; cytostatic; vaccine;  
 XX gene therapy.  
 OS Homo sapiens.  
 XX  
 PN WO2003100000-A2.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PR 24-MAY-2002; 2003US-0392656P.  
 XX  
 DR 25-JUL-2002; 2002US-0398099P.  
 XX  
 PA (TULA-) TULARIK INC.  
 XX  
 PT Li J, Mu D, Yang J;  
 XX DR WPI; 2004-035118/03.  
 DR N-FSDB; ADP83102.  
 GENBANK; NP\_065702.  
 XX  
 PT Diagnosing a cancer in a mammal comprises determining RecQL5, CTRIL, USP13, MCL1 or Pellino 1 gene copy number in a biological sample from a  
 PT region of the mammal that is suspected to be precancerous or cancerous..  
 XX  
 PS Claim 179; SEQ ID NO 10; 174pp; English.  
 XX  
 CC The present sequence is the protein sequence of human Pellino homologue 1  
 CC (Pellino), a protein associated with the kinase domain of activated  
 CC Pellino. The invention is based on the finding of the overexpression of  
 CC Pellino and other genes (RecQL5, CTRIL, USP13 and MCL1) in certain  
 CC cancers, including breast cancer, colon cancer, lung cancer and ovarian  
 CC cancer, and the frequent amplification of these genes in cancer cells.  
 CC The genes, and their expression products, can be used diagnostically or  
 CC as targets for cancer therapy. They can also be used to identify and  
 CC design compounds useful in the diagnosis, prevention and therapy of  
 CC tumours and cancers, in vaccine development and in methods for  
 CC determining the efficacy of a treatment regime. A claimed method for  
 inhibiting cancer or precancerous growth, especially in ovarian or lung  
 CC tissue, uses an inhibitor that interacts with Pellino1 DNA or RNA. The  
 CC inhibitor is a small interfering RNA (siRNA), microRNA (miRNA), an  
 CC antisense RNA, and antisense DNA, a decoy molecule, a decoy DNA, a  
 CC ribozyme or small molecule.  
 XX  
 Sequence 418 AA:  
 SQ Query Match 83.7%; Score 1917; DB 8; Length 418;  
 Best Local Similarity 81.4%; Pred. No. 7.4e-188;  
 Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;  
 QY 1 MFSPGQEHCAPNKEPKVKGELVWGLNGALPENGDRGRKSRAKYKPKANGVKPVSTVH 60  
 Db 1 MFSPGQEHCAPNKEPKVKGELVWGLNGALPENGDRGRKSRAKYKPKANGVKPVSTVH 58  
 QY 61 VISTPOASKAISCKQHSISYTTSRNSQTVWVTHDKOTDMQVGRSTESPDPFWVTI 120  
 Db 59 IACTPOAKAISKDHSISYTTSRASQTVWVTHDSNIDMEQIGRSIESPDPFWVTI 118  
 QY 121 SGSONTDAQITOSTISFACRVCDRNPYTAIFAGFDSSKNIFGKAKWKPSDG 180

Db	119 PSSQSNSTQSVOSTISRFACRICERCPPFTARIYAGFDSSKNIFGEKAKWKTSD	CC
Ov	181 HMDGLITNGVLUHMPRGFTESQPGWREISVGDVYTTRSAORGKLVESETNVL	CC
Db	179 QDSSLIDCGATULWRDGLFTPTQHIEALRQEINARQCPVNTLAFPSINKE	CC
Ov	241 QDSSLIDCGATULWRDGLFTPTQHIEALRQEINARQCPVNTLAFPSINKE 300	CC
Db	239 QDSSLIDCGATULWRDGLFTPTQHIEALRQEINARQCPVNTLAFPSINKE 298	CC
Ov	301 VWEKOPMAYLSCHVHGTYHNGHSRDTBANEERECPMRTVGPVPLGCEAGFYTDAG	CC
Db	299 VWEKOPMAYLSCHVHGTYHNGHSRDTBANEERECPMRTVGPVPLGCEAGFYTDAG	CC
Ov	361 PPTHAFTPCGHVSEKSAKWSQIPLPHGTHAFCACPCATOLQVGEONCILKIFQPID 420	CC
Db	359 PPTHAFTPCGHVSEKTAWSQIPLPHGTHAFCACPCATOLQVGEONCILKIFQPID 418	CC
<b>RESULT 14</b>		
ID	ADO44005 standard; protein; 418 AA.	
XX		
AC	ADO44005;	
XX		
DR	15-JUL-2004 (first entry)	
XX		
DB	Amino acid sequence of human Pellino 1.	
XX		
KW	Wallerian degeneration; Alzheimer's disease; neurological disorder; epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease; atherosclerosis; 1D-myo-inositol triphosphate 3 kinase A; ASK1; ASK2; Ask3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha; Cdc37; CHK2; CICL tumour antigen SE20-4; EF-1 alpha 1; ENAP; FBL14653 NTZRP200225; FLJ0839 FEBR2002429; HERC2; inositol polyphosphate-5-phosphatase; inositol-1,4,5-triphosphate 5-phosphatase type 1; IAK1; IAK4; KIAA41; MSTP030; Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1; Pushover; S-adenylylhomocysteinase; secretory carrier-associated membrane protein 2; surfactin locus protein 2; ubiquitin carboxyl terminal hydrolase 11; upstream regulatory element binding protein 1; Vartul; Werner's syndrome helicase interacting protein 4 (isoform 1). The present sequence represents Pellino 1.	
XX		
SQ	Sequence 418 AA;	
XX		
DR	Query Match 83.7%; Score 1917; DB 8; Length 418; Best Local Similarity 81.4%; Pred. No. 7.4e-188; Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1; Matches 342; Conservative 38; Mismatches 38; Indels 2; Gaps 1;	
XX		
Ov	1 MFSPGQEBHCAPNEKEPVKGELVNGALENGDRRRKSRAFPKANGVKESTVH	CC
Db	1 MISPDQETH- -PSKAPKPYGEJLVNGSLNGDRGRKRSPALPKRKANGVKESTVH	CC
Ov	61 VISTPOASKAISCKGQHISYSUTSRNOMTVVYTHDKDTDMFOVGSTESPIDFWVTDTI	CC
Db	59 IACTPOAKAISKQHISYSUTSRNQTVVYTHDSNTDWQIGRSTESPIDFWVTDTI	CC
Ov	121 SESQNTDEAQQTOSTISRFACRICERCPPFTVPEYTAIFAGEFSSKTFGEKAKWKTSD	CC
Db	121 SESQNTDEAQQTOSTISRFACRICERCPPFTVPEYTAIFAGEFSSKTFGEKAKWKTSD	CC
Ov	119 PGSQNSNTQSVOSTISRFACRICERCPPFTARIYAGFDSSKNIFGEKAKWKTSD	CC
Db	119 PGSQNSNTQSVOSTISRFACRICERCPPFTARIYAGFDSSKNIFGEKAKWKTSD	CC
Ov	181 HMDGLITNGVLUHMPRGFTESQPGWREISVGDVYTTRSAORGKLVESETNVL	CC
Db	179 QDSSLIDCGATULWRDGLFTPTQHIEALRQEINARQCPVNTLAFPSINKE	CC
Ov	241 QDSSLIDCGATULWRDGLFTPTQHIEALRQEINARQCPVNTLAFPSINKE 300	CC
Db	239 QDSSLIDCGATULWRDGLFTPTQHIEALRQEINARQCPVNTLAFPSINKE 298	CC
Ov	301 VWEKOPMAYLSCHVHGTYHNGHSRDTBANEERECPMRTVGPVPLGCEAGFYTDAG	CC
Db	299 VWEKOPMAYLSCHVHGTYHNGHSRDTBANEERECPMRTVGPVPLGCEAGFYTDAG	CC
Ov	361 PPTHAFTPCGHVSEKSAKWSQIPLPHGTHAFCACPCATOLQVGEONCILKIFQPID 420	CC
Db	359 PPTHAFTPCGHVSEKTAWSQIPLPHGTHAFCACPCATOLQVGEONCILKIFQPID 418	CC
<b>RESULT 15</b>		
ID	ADP48667 standard; protein; 418 AA.	
XX		
AC	ADP48667;	
XX		
DT	05-SEP-2004 (first entry)	
XX		
DE	Human Pellino-1 protein SSO ID NO:4.	
XX		
PT	Bouwmeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;	
XX		
PI	Kroeser B, Hopf C;	
XX		
DR	WBI; 2004-316467/29.	
XX		
PT	New complex comprising at least one first protein, and at least one second protein, useful for treating stroke, Alzheimer's disease, neurological disorders such as epilepsy, and inflammatory conditions such as ulcerative colitis.	
XX		
PS	Example: Page 224-226; 287pp; English.	
XX	The specification describes protein complexes involved in cellular	
CC	processes which have been shown to be critical for the development of various forms of neurological diseases. Three protein complexes were identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3 protein complex. The protein complex are useful for treating diseases and disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration, Alzheimer's disease, inflammatory conditions such as ulcerative colitis, Crohn's disease or atherosclerosis. Proteins identified as being part of the protein complexes of the invention are 1D-myo-inositol triphosphate 3 kinase A, ASKL, ASK2, ASK3, Camkii beta, Camkii delta, Camkii gamma, casein kinase II alpha, Cdc37, Chk2, Crg1, tumour antigen S200-4, Ef-1 alpha 1, Bmp, Flj14583 Ntzrp2002252, Flj0839 FEBR2002429, Herc2, two hypothetical proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase, inositol-1,4,5-triphosphate 5-phosphatase type 1, Iak1, Iak4, KIAA41, Mstp030, Nek9, Par3, Pellino 1, Pellino 3, podocalyxin-like protein 1, precursor, Pushover, a putative S-adenylylhomocysteinase, secretory carrier-associated membrane protein 2, surfactin locus protein 2, ubiqutin carboxyl terminal hydrolase 11, upstream regulatory element binding protein 1, Vartul, Werner's syndrome helicase interacting protein 4 (isoform 1). The present sequence represents Pellino 1.	
XX		
CC	nuclear factor kappa B dependent transcription inhibitor; NF-kB-dependent transcription inhibitor; Pellino-1; p38-dependent transcription inhibitor; Pellino-1; interleukin 1 receptor-associated kinase 4; Iak-4; antiarteriosclerotic; antiarthritic; antiasthmatic; antiinflammatory; antirheumatic; antiulcer;	

XX KW gastrointestinal; neuroprotective; nootropic; IL-1 antagonist;  
 XX IRAK protein kinase family inhibitor;  
 XX NF kappa B inducing kinase inhibitor; asthma; rheumatoid arthritis;  
 XX inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 XX atherosclerosis; Alzheimer's disease; human; chromosome 2.  
 XX OS Homo sapiens.  
 XX PN WO2004053092-A2.  
 XX PD 24-JUN-2004.  
 XX PR 09-DEC-2003; 2003WO-US039188.  
 XX PR 11-DEC-2002; 2002USN-00317250.  
 PA (IMMUNEX ) IMMUNEX CORP.  
 PA (CLEV-) CLEVELAND CLINIC FOUND.  
 XX PI Bird TA, Cobman DJ, Li X;  
 XX DR WPT; 2004-480927/45.  
 XX DR N-PSDB; ADP48666.  
 XX PT Identifying inhibitors of IL-1 signaling, useful for treating e.g.,  
 XX asthma and rheumatoid arthritis, comprises assaying the association of  
 XX the Peillin-1 polypeptide with IRAK-4 in the presence of a test compound.  
 XX PS Claim 8; SEQ ID NO 4; 81pp; English.  
 CC The present invention describes a method for identifying compounds (C)  
 CC that inhibit nuclear factor kappa B (NF- $\kappa$ B)-dependent transcription or  
 CC p38-dependent transcription. The method comprises: (1) mixing a test  
 CC compound with a Peillin-1 polypeptide; (b) assaying the association of  
 CC the Peillin-1 polypeptide with IL-1 receptor-associated kinase 4 (IRAK-  
 CC in the presence of the test compound; and (c) determining whether the test  
 CC compound inhibits the association of the Peillin-1 polypeptide with  
 CC a binding partner. Also described: (1) an inhibitory nucleic acid that  
 CC binds to a nucleic acid encoding an amino acid sequence as described  
 above, where the presence of the inhibitory nucleic acid within a cell  
 CC inhibits the association of Peillin-1 with IRAK-4; and (2) an inhibitor  
 CC polypeptide comprising an antibody fragment that binds to a polypeptide  
 CC comprising an amino acid sequence as described above, where the presence  
 CC of the inhibitory polypeptide within a cell inhibits the association of  
 CC Peillin-1 with IRAK-4. (C) have antiarrheoic/coleretic, antiarthritic,  
 CC antiasthmatic, antiinflammatory, antirheumatic, antiulcer,  
 CC gasterointestinal, neuroprotective and nootropic activities, and can be  
 CC used as an IL-1 antagonist, IRAK protein kinase family inhibitor, and NF  
 CC kappa B inducing kinase inhibitor. The methods and compositions of the  
 present invention are useful for the prevention and/or treatment of  
 CC diseases or conditions associated with aberrant expression or activity  
 CC of the Peillin-1 polypeptide, such as asthma, rheumatoid arthritis,  
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,  
 CC atherosclerosis and Alzheimer's disease. The present sequence represents  
 CC human Peillin-1, which is used in the exemplification of the present  
 invention. The human Peillin-1 gene is located on chromosome 2, more  
 CC specifically to 2p13.3.  
 Sequence 418 A;

Search completed: March 1, 2006, 20:56:04  
Job time : 187 secs

Query	Match	83.7%	Score	1917	DB	8	Length	418;
Best Local Similarity	81.4%	Pred.	No.	7	4e-188;			
Matches	342;	Conservative	38;	Mismatches	38;	indels	2;	Gaps
Oy	1	MFSRPOBERHCPNPKPVKGILVULGNGALINGDRGRKRSRFPALYKRPKANGWKPSVH	60					
Db	1	MFSRPOENH - PSKAIVKGILVULGNGALINGDRGRKRSRFPALYKRPKANGWKPSVH	58					
Oy	61	VISTQASKALSKGHSISYTLRIQTYWYETHDKDITDMQVGRATESPDPWYDTI	120					
Db	59	IACTPOAKAISNKDOHSISYTLRAOTUVVWXTHDNTDMQIGRSTESPIDFWVTDTI	118					
Oy	121	SGSONDRAOTOSTSRPAPTCVCPNRPYATRAGFDSKNTFRGKAKWKG	180					

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